

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 96506

TO: Sheridan Swope

Location: cm1/12d12/10d01

Art Unit: 1652

Friday, June 20, 2003

Case Serial Number: 966880

From: Paul Schulwitz

Location: Biotech-Chem Library

CM1-6B06

Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (703)305-1954



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BO055935 AGENCOURT T06576 EST04465 Fe AG056000 Pan trog1 AW303243 xr90c01.x AB181647 tw44c03.x BF806490 RC0-CIO03 BE177917 RC3-HT060 AW562095 SWOVAFCAP AA937809 nw89b02.s BE169901 CW0-HT052 AA5867246 nn39all.s AA769235 nm31al0.s AW799144 RC0-UM005 AQ055921 HS_5313_B AQ055921 HS_5313_B AQ055921 HS_5313_B AQ055921 HS_5313_B AQ055921 HS_5313_B AQ05791 RC0-UM005 BE151155 RC4-HT027 AL601949 DKFZp313D BE151208 RC4-HT027 AL601949 DKFZp313D BE15115 RC4-HT027 AQ389816 RC4-HT027 AQ389816 RC4-HT027 AQ389816 RCC111-14 BC621190 602616889 AQ379336 RPCH11-92 AG15837 Pan trog1 AQ178815 Pan trog1 AG173021 Pan Trog1 AG1

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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Other_GSSs: CIT-HSP-2326M11.TV

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                         sequence.
AQ042682
AQ042682.1
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                                                                                                                                                                                                                                                        AQ042682 293 bp DNA linear GCIT-HSP-2326M11.TR CIT-HSP Homo sapiens genomic clone
Clones are available end search page:
        Fax: 301 030 CE Email: mdadams@tigr.org
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AA9033793
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AQ559921
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           Research Genetics (info@resgen.com).
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GSS 14-JUL-1998 ne 2326MII, bwa

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REFERENCE
AUTHORS
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                                                                                                               Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be
                                                                   http://image.llnl.gov
Plate: LLCM1694 row: k column:
High quality sequence stop: 693.
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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Seq primer: M13 Reverse
Class: BAC ends.
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/db_xref="taxon:9606"
/clone="IMAGE:4851580"
                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Best Local :
                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM895 row: p column: 20
High quality sequence stop: 541.
Location/Qualifiers
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1 (bases 1 to 541)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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87; Conserv
                          120
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
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Site_2: EcoR1; clNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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ilarity 100.0%;
Conservative
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXhoI sites using the following 5' adaptor: GGCACGAGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 743)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates;
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  CACTCTGGACACCACTATGGACAG 85
                                                                                GAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGGGAGGCAAGAAGA
                                                                                                                                                          1.5%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                    /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
76 a 197 c 188 g 182 t
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/db_xref="taxon:9606"
/clone="IMAGE:4766234"
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100.0%; Pred. No.
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Pred. No.
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Mismatches
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5', mRNA sequence.
BQ065440
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian
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602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639
                  Homo sapiens
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                                         human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="NIH_MCC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:4335639"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0,;

Indels

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Gaps

linear

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                         cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                              NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 1052)
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AGENCOURT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808181
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Plate: LLCM2108 row: P column: 10
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lou Staudt
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/ob_xrefe"taxon:9606"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
/clone="IMAGE:5929977"
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/lab_host="DHOB (phage-resistant)"
/note="Organ: lymph; Vector: pOTBF; Site_1: XhoI; Site_2:
Into EcoRI; XhoI sites using the following 5; adaptor:
Into EcoRI;XhoI sites using the following 5; adaptor:
1.8kb Library constructed by Ling Hong in the laboratory
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
IRT (Life Technologies). Note: this is a NIH_MGC
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The Institute for Genomic Resear
932 Clopper Road, Gaithersburg,
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Gene
93364420
                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
Seg primer: M13-21
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1 (bases 1 to 423)

Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.

3,400 expressed sequence tags identify diversity of transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from human brain
Nat. Genet. 4, 256-267
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423 bp mRNA linear EST 30-JUN-1993 EST04465 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA-clone HFBDV37 similar to EST containing Alu repeat, mRNA sequence.
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                                         95 a
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Plate: LLCM2051 row: m
/Organism="Homo sapiens"
/db_xref="ATCC (inhost):83234"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="HFBDY37"
/clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Yector: LambdaZAP-II; 17-18 wk gestation, femoligo-dT + random primed cDNA synthesis; lambdaZAP-I vector, 1.0kb average inser size."
95 a 109 c 96 g 117 t 6 others
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/clone_1ib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymphoma, vector: poTBF; Site_1: xho; Site_2:
/note="Organ: lymph; Vector: poTBF; Site_1: xho; Site_2: x
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/db_xref="taxon:9606"
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RESULT 7 BQ055935

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ORIGIN BASE COUNT

FEATURES

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REFERENCE TITLE JOURNAL AUTHORS

Query Match Best Local

Matches

COMMENT

female;

us-09-966-880a-9.oli.rst

/sex="mate" //cell_type="lymphoblast" //celne_lib="PTB Chimpanzee Male BAC Library" //celne_library	PRIMENS Sequencing: M13Rev Sequencing: M13Rev LIBRARY LIBRARY Vector : pKS145 Vector : SacI R. Site 1 : SacI R. Site 2 : SacI R. Site 2 : SacI Location/Qualifiers Location/Qualifiers fearures 1 . 648 Joganism="Pan troglodytes" /objarism="pan troglodytes" /objarism="pan troglodytes" /clone="ptp-042C11.R"	TITLE Direct Submission Direct Submission JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan and Chemical Research (RIKEN), Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suchiro-chimpheségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, (E-mail:chimpheségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end Tel:181-45-503-9111, Fax:81-45-503-9170) COMMENT was generated during the R&D process and may have higher chance of clone tracking errors.	WE SO THE	SULT 9 056000/c AG05 CUS PAN CUS PAN CUSSION PAN CUSSION AG05 CHESION AG05 CHESION AG05 CHESION AG05 CHESION AG05	Query Match Best Local Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0; Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0
RESULT 11 A1811647 I.OCUS DEFINITION TW44C03.x1 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2262532 3' LOCUS DEFINITION TW44C03.x1 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2262532 3' LOCUS DEFINITION LOCUS ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM EST. Homo sapiens EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo. Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Manmalia; Locus MCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	68; CONSERVATIVE O, PROPERTY OF THE CATCHIST O	adenocarcinoma tissue, cDNA made Dy Olly Olly adenocarcinoma tissue, cDNA made Dy Olly Olly Olly Olly Olly Olly Olly O	www-bio.llnl.gov/pur// arys- seq primer: -40up from clbco Seq primer: -40up from clbco Seq primer: -40up from clbco High quality sequence stop: 424. High quality seq	TIFLE Tumor Gene Index Tumor Gene Index JOURNAL Unpublished (1997) COMMENT Email: cgapbs-r@mail.nih.gov Email: consortium, LLNL cDNA Library Arrayed by: I.M.A.G.E. Consortium/LLNL Email: claribution: NCI-CGAP clone distribution information can be DNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	RESULT 10 AW303243 COCUS DEFINITION SIGNATURE AW303243 ACCESSION VERSION VERSION KEYWORDS ORGANISM EMBA ORGANISM EMBA ORGANISM EMBA AW303243 AUTHORS ORGANISM EMBA ORGANISM ORGANIS

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Dlas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                      sequence.
BF806490
                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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RCO-CI0037-081100-032-d01_1 CI0037
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Contact: Robert St
                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Mammalia;
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                           sequence tags
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Prof. Antonio Prudente 109,
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                                                                                        Natl. Acad. Sci. U.S.A.
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/clone_lib-"NCI_CGAP_Utl"
/tissue_type-"well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                        Eutheria;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Matsukuma, A., Bala, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCOst2=RCO-CI0037-081100-032-001_ist3=2000-11-08st4=1) seq primer: puc 18 forward High quality sequence stop: 164.
                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2-RC3-HT0600-170
300-011-901_1&t3=2000-03-17&t4=1)
                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea;
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Lizotte-Waniewski, M. and Williams, S.A.
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/sex="temaie"
//dev_stage=adult"
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//lab_host="XLI-Blue MRF'"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco RI; Sit
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/clone_lib="Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Onchocerca volvulus"
/db_xref="taxon:6282"
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/clone_lib="HT0600"
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5446 TTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 5505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 TITGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray,
Tissue Procurement: W. Douglas Figg, Ph.D., Ph.C. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution informatio
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nw89b02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone TM similar to contains Alu repetitive element; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repetitive element ;, mRNA sequence.
                                                                  Similarity 100
57; Conservative
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                                                                                                                                                                                                                                                 /note-"Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is availy from Dr. Steven A. Williams, email: genome@smith.edu." a 60 c 80 g 48 t
                                                                                                                                                                                                                              average insert size 600 bp.
                                                                                                                                                                                                                                                                                                                      /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1253739"
/clone_lib="NCI_CGAP_Pr12"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No.
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Db	Оу
	5506 ACCTCAG 5512
	228 ACCTCAG

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Command line parameters:

-MODEL-frame+_n2p.model -DEV-xlp
-MODEL-frame+_n2p.model -DEV-xlp
-O-/cgn2_1/USPTO_spool/US09966880/runat_14062003_175621_11081/app_query.fasta_1.5703
-DB-PIR_73 -OFMT-fastan -SUFFIX=Olin2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MATRIX=Oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto
-NORM-ext -HEAPSIZE=500 -MINLEN0-0 -MAXLEN-2000000000
-USER-US09966880_eCGN_1_1_274_erunat_14062003_175621_11081 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPDP=60 -XGAPDP=6
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Maximum
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Perfect score:
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1: pir1:
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Match
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B40201	T09075	в29653	I52523	T49559	S46716	S30850	S55141	D90517	C86477	A71615	JN0263	T18440	E71615	F71608	A96788	T18446	T18439	F71619	T46395	T52355	н84730	S38112	T18513	S64364	I79424	A38420	A40201	A40201	E40201	E40201	
	hypothetical prote	'n.		_				hypothetical prote	protein F1504.29 [antigen (clone PV1	hypothetical prote		hypothetical prote	Η	-	_	_		hypothetical prote		hypothetical prote	hypothetical prote	probable membrane	MHC HLA-DR-beta-1	antifreeze glycopr		artifact-warning s		artifact-warning s	

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ALIGNMENTS

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hypothetical ORF near NoS2 locus - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 08-Apr-1998 #text_char
A; Title: Locus for the inducible, but not a constitutive, nit
A; Title: Locus for the inducible, but not a constitutive, nit
A; Reference number: I55615; MUID:95256440; PMID:7537756
A; A; A; Ccession: I55615
A; Ccession: I A;Cross-references: EMBL:U16359; NID:g854726; PIDN:AAC52199.1; C;Comment: This is the hypothetical translation of a sequence tC;Keywords: cloning artifact RESULT Alignment Scores: 08-Apr-1998 #text_change 19-May-2000 not nitric shown; PID:g854727 believed to oxide translated synthase contain from coseg

GB/

clo

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RESULT 2
148725
Q300 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revisio
C:Accession: I48725
                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                    US-09-966-880A-9 (1-5514) x I55615
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15.00
100.00%
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Matches:
Conservative:
Mismatches:
Indels:
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#sequence_revision

02-Jul-1996 #text_change

05-Nov-1999

exons by similarity search: MUID:92241891; PMID:1572661

Alu-derived

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other

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A;Reference number: A A;Reference number: A A;Accession: F40201 A;Molecule type: DNA A;Residues: 1-673 <CL.
R;Claverie, J.M.
                                                                                                            artifact-warning sequence (translated / C:Species: Homo sapiens (man) C:Date: 31-Mar-1992 #sequence_revision C:Accession: F40201 R:Claverie, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-296 <CAI>
A; Cross references: EMBL:X12544; NID:g32210; PIDN:CAA31061.1; PID:g32211
A; Cross references: EMBL:X12544; NID:g32210; PIDN:CAA31061.1; PID:g32211
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1988
A; Note: the nucleotide sequence is given
A; Note: the authors translated the codon TTT for residue 266 as Gly
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
F; 1-29/Domain: signal sequence #status predicted <SIG>
F; 30-296/Product: class II histocompatibility antigen, HLA-DR beta-1 chain #status
F; 139-204/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                        RESULT
F40201
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Query
DB:
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A;Title: Identification of a novel DR beta cDNA clone.
A;Reference number: S01441; MUID:89016649; PMID:3174462
A;Accession: S01441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
$01441
Class II histocompatibility antigen HLA-DR beta-1 chain precursor (clone LS: C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000 C;Accession: $01441
C;Accession: $0141 C.A.; Curtsinger, J.M.; Bach, F.H.
                                                                    R;Claverie, .... personal communication, 19
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Query Match:
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J. Title: The Q300 gene: a novel trans.
                                                                                                                                                                                                                                                                                                                                  US-09-966-880A-9 (1-5514) x S01441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores: Pred. No.:
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A; Residues: 1-77 < RES>
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C:Accession: S57138
C:Accession: S57138
R:Rose, M.; Koetter, P.; Entian, K.D. submitted to the Protein Sequence Dat
C;Genetics:
A;Gene: MIPS:YJR115w
A;Cross-references:
A;Map position: 10R
                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision
C;Accession: S57138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Leishmania major
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2002
C;Accession: T18321
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T18321
                                         A;Cross-references:
C;Genetics:
                                                                       A; Molecule type: DNA
A; Residues: 1-169 < R
                                                                                                                                                                                                      hypothetical protein YJR115w - N; Alternate names: hypothetical
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Query Match:
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A; Residues: 1-169
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Best Local Similarity:
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C;Comment: This "warning" entry is a c
in-frame stop codons are shown as 'X'
C;Comment: Any significant similarity
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                                                                       <ROS>
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               SGD:S0003876
                                                         EMBL: 249615;
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L protein J2027
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                                                        NID:g1015832;
                                                                                                                                Database,
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision
C;Accession: C40201
Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation
in-frame stop codons are shown as 'X'
C;Comment: Any significant similarity of a predicted protein
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C40201
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Best Local Similarity:
Query Match:
DB:
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A; Residues: 1-301 <CLA>
R; Residues: 1-301 <CLA>
R; Claverie, J; M;
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived
A; Reference number: A40200; MUID:92241891; PMID:1572661
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Best Local Similarity:
Query Match:
DB:
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personal communication, 19
A:Reference number: A40201
A:Accession: C40201
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C;Comment: Any significant similarity of a predicted protein
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C; Date: 31-Mar-1992 #sequence
C; Accession: B40201
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Pred. No.:
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A; Residues: 1-613 <CLA>
R; Claverie, J.M.
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A; Reference number: A40201
A; Accession: B40201
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Alignment Scores:

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A; Molecule type: DNA
A; Residues: 1-6.13 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding e
A; Reference number: A40200; M
                                                                                                                                                                                A:Experimental source: adult testis; C;Genetics:
                                                                                                                                                                                                                                                          hypothetical protein DKFZp434G1035.1 - C;Species: Homo sapiens (man) C;Date: 11-Jan-2000 #sequence_revision
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C;Comment: Any significant similarity of a predicted protein
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Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
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A;Residues: 1-163 <AAAA>
A;Cross references: EMBL:AL133039
                                                                                                                                                                                                                                 C;Accession: T42696
R;Poustka, A.; Klein, M.; Mewes, H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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A; Accession: C40201
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C;Species: Homo sapiens (man)
C;Date: 31-Mar_1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
                                                                                                                                                                            A; Status: preliminary
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Matches:
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Percent Similarity:
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A:Experimental source: strain UAB CTIP
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                  R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucleic Acids Res. 29, 2145-2153, 2001)
A:Title: The complete genome sequence of the murine respiratory A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: C90517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 *sequence_revision 24-May-2001 *text_change 03-Aug-2001
C;Accession: C90517
R;Chambaud, I; Hellig, R.; Ferris, S; Barbe, V.; Samson, D.; Galisson, F.
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preá
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A; Residues: 1-296 < KUR>
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A; Experimental source: BAC clone B208;
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A; Residues: 1-230 <SCH>
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A; Accession: T49555
                                          US-09-966-880A-9 (1-5514) x C90517
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208; strain OR74A
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A; Rolecule type: mRNA
A; Residues: 1-515 < ABE>
A; Cross-references: EMBL: X64429; NID: g11063; PIDN: CAA45771.1;
A; Cross-reference extracted from NCBI backbone (NCBIP: 88160)
                                                                                                                                                                                                                                                                                                                                   A; Status, recent type: mRNA
A; Molecule type: mRNA
A; Residues: 1-516 <SMO>
A; Cross references: GB: M87038; NID: g157118; PID: g157119
A; Cross references extracted from NCBI backbone (NCBIN: 111718,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Cell. Biol. 12, 4123-4131, 1992
A;Title: A cyclic AMP-responsive element-binding transcriptional
A;Reference number: A44494; MUID:92375081; PMID:1508208
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A;Title: A Drosophila CREB/ATF transcriptional activator A;Reference number: A42140; MUID:92192458; PMID:1532159 A;Accession: A42140
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C;Date: 04-Mar-1993 #sequence_revision
C;Accession: A42140; S24542
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Query Match:
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C;Superfamily: fos/jun DNA-binding domain homology
F;433-476/Domain: fos/jun DNA-binding domain homology
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C;Species: Drosophila melanogaster
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change C
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C;Superfamily: fos/jun DNA-binding domain homology
C;Keywords: DNA binding; nucleus; transcription regulation
C;Keywords: DNA binding; nucleus; transcription cyulation
F;432-475/Domain: fos/jun DNA-binding domain homology <FJD:
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Artifact warning sequence (translated ALU class E) - human c:Species: Homo saplens (man) c:Date: 31-Mar-1922 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 c:Accession: BiO201

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APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
US-09-978-197-3
US-09-750-580-1
US-09-791-211-10
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-09-341-9278-1
US-08-531-9278-1
US-08-531-9278-1
US-08-481-520
US-08-481-53-20
US-08-481-5548-20
US-08-488-0118-20
US-08-488-0118-20
US-08-488-0118-20
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Clinton Square, P.O. Box 1051
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN 5USAN J. 103
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2089
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716,263-1636
TELEPHONE: (716,263-1636
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TELEFAX: (716) 23-160
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 20303 base pairs TYPE: nucleic acid
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Best Local Similarity 100.0
Matches 67; Conservative
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RY: USA
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STREET: Cli
CITY: Roche
STATE: New
COUNTRY: US
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Sequence 1, Appli
Sequence 1, Appli
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7828.776 Million cell updates/sec
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Sequence 382,
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                                                                                                                                             June 19, 2003, 07:46:55; Search time 216 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-832-883-49
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US-09-301-665-3
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US-09-089-595-3
US-09-382-855-3
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US-09-735-934A-3
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US-08-475-352-1
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Perfect score:
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Maximum DB
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                                                                                                                                       TYPE: DNA
ORGANISM: Human
   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-798-096-10/c
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                                                                                               SEQ ID NO 3
LENGTH: 8758
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ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
THEREOF
6392 TTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 6451
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                                                                                                                                                                                                                             APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Raren X.B.
ATILE OF INVENTION: Human Deoxycytidylate Deaminase Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
FILING DATE: 10-JAN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20894/80
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716,263-1636
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         Sequence 1, Application US/08370975B Patent No. 5622851
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Patent No. 6323016
Patent Nerormation:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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TYPE: nucleic acid
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                                     5506 ACCTCAG 5512
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COUNTRY: USA
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US-09-799-345-3
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APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Stefan: Reed, Daryl
TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor
TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
TITLE OF INVENTION: Antibodies Specific To The Molecule, and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
FILE REPERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
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1.2%; Score 66; DB 4; Lo
Best Local Similarity 100.0%; Pred. No. 6.9e-16;
Matches 66; Conservative 0; Mismatches 0;
                                                                                 FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/799,345
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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Hanson, No. 6153728man D.
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US-09-382-855-3
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US-09-382-855-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
APPLICANT: Stefan; Reed, Daryl
TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
TITLE OF INVENTION: Antibodies Specific To The Molecule, and
TITLE OF INVENTION: Oses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEB: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 61; DB 2; Length 2559;
100.0%; Pred. No. 6.1e-14;
tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,774B
FILING DATE: 03-October-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY AACENT INFORMATION:
NAME: Hanson, No. 5908778man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,595
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                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2559 nucleotides
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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Matches 61; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
New York
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                                                                                                     COMPUTER: IBM
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US-09-089-595-3
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Sequence 3, Application US/09382855
Patent No. 6174692
GENERAL INFORMATION:
APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
APPLICANT: Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor Rejection
TITLE OF INVENTION: Antigen Precuros Mage-10, Antibodies Specific To The Molecu CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        5452 TTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCA 5511
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                                                                                                                                                                                                                                                                                                                                Length 2559;
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                                                                                                                                                                                                                                                                                                                                1.1%; Score 61; DB 3; L
100.0%; Pred. No. 6.1e-14;
tive 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,855
FILING DATE: 25-August-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/089,595
FILING DATE: 02-June-1998
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/724,774
FILING DATE: 03-October-1996
CLASSIFICATION: 435
             REFERENCE/DOCKET NUMBER: 20,340
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 888-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2559 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Schofield, Mary Anne
REGISTRATION NUMBER: 36,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEPAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2559 nucleotides
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Best Local Similarity 100.0
Matches 61; Conservative
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STRANDEDNESS: single
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: New York
RY: USA
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MEDIUM TYPE: Diskett
COMPUTER: IBM
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                          linear
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Sequence 3, Application US/09735934A

Patent No. 6372468

GENERAL INFORMATION:
APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT APPLICATION NOMBER: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5452 TTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCA 5511
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                                                                                            APPLICATION NUMBER: US 09/089,595
FILING DATE: 02-June-1998
APPLICATION NUMBER: US 08/724,774
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Schofleld, Mary Anne
REGISTRATION NUMBER: 36,669
REGISTRATION NUMBER: LUD 5457.2 DIV - J
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 752-5958
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 1.1%; Score 61; DB 4; Ler
Local Similarity 100.0%; Pred. No. 3.8e-14;
nes 61; Conservative 0; Mismatches 0;
               APPLICATION NUMBER: US/09/642,281
FILING DATE: 18-Aug-2000
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2559 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ORGANISM: Homo sapiens
US-09-735-934A-3
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US-09-735-934A-3/C
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LENGTH: 43950
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Matches
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5183884-1
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TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor Rejection
Antigen Precuros Mage-10, Antibodies Specific To The Molecu
                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09183714B

Patent No. 6221593

GENERAL INFORMATION:
APPLICANT: Brasseur, Francis
APPLICANT: Brasseur, Francis
APPLICANT: Brasseur, Francis
APPLICANT: Brasseur, Etienne
TITLE OF INVENTION: Method for Determining Cancer by Determining Expression
TITLE OF INVENTION: of MAGE-10
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/183,714B
CURRENT FILING DATE: 1998-10-30
FRIOR APPLICATION NUMBER: US 08/724,774
PRIOR FILING DATE: 1996-10-03
FRIOR ELING DATE: 1996-10-03
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                                                          Gaps
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Patent No. 6387698
GENERAL INFORMATION:
APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
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                   Length 2559;
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100.0%; Pred. No. 6.1e-14;
tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
    DB 4; Leus, 6.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 66 Fifth Avenue
CITY: New York City
STATE: New York
               1.1%; Score 61; DB 100.0%; Pred. No. 6.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
            Query Match 1.1
Best Local Similarity 100.
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                     2262 G 2262
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LENGTH: 2559
                                                                                                                                                                                                                                                                                                          US-09-183-714B-3
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US-09-642-281-3
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Gaps

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Sequence 1, Application US/08473119
Sequence 1, Application US/08473119
Patent No. 5820859
GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: Aaronson, Stuart A.
TITLE OF INVENTION: BIOARED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: BIOASSAYS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: Suite 400
STREET: 133 Carnegle Way, N.W.
CITY: Atlanta
CITY: Georgia
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                         Query Match 1.1%; Score 60; DB 1; Length 1542; Best Local Similarity 100.0%; Pred. No. 1.5e-13; Matches 60; Conservative 0; Mismatches 0; Indels
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,119
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,895
FILING DATE: 10-NOV-1992
ATTOMORALE: 01-DEC-1989
ATTOMORALE: US-DEC-1989
ATTOMORALE: DEC-1989
                                                                                                                                                                                              join(66..221, 780..855, 1040..1185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFRENCE/CDCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TRIEFEX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  1040..1185
                                                                                                            intron
856..1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                    FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-07-978-895-1
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FEATURE:
  LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kraus, Matthias H.
APPLICANT: Kraus, Matthias H.
APPLICANT: Astonom, Stuart A.
APPLICANT: Astonom, Stuart A.
TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: BIDBERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND
TITLE OF INVENTION: BIOASSAXS AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 400
STREET: 133 Carnegie Way, N.W.
                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                             Length 1541;
                                                                                                                                                                                                                                                                                                    0; Indels
               APPLICANT: KRAUS, MATTHIAS H.; AARONSON, STUART A.
TITLE OF INVENTION: DNA SEGMENT ENCODING A GENE FOR A.
FRECEPTOR RELAPED TO THE EPIDERWAL GROWTH FACTOR RECEPTOR
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/444,406
FILLING DATE: 01-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PURDAGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,895
FILING DATE: 19921110
CLASSIFICATION: 435
PROR APPLICATION NUMBER: US 07/444,406
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: PETYMAN, DATA:
NAME: PETYMAN, DAY1G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1144-028
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           1.1%; Score 60; DB 6; I
100.0%; Pred. No. 1.5e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07978895
Patent No. 5480968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TELEPAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
                                                                                                                                                                                                                                                         Query Match 1.1%
Best Local Similarity 100.0°
Matches 60; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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: U.S.A.
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STATE: Georgia
                                                                                                                                                                                            LENGTH: 1541
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ZIP: 30303
; Patent No. 5183884
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                                                                                                                                                                     ; SEQ ID NO:1:
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NAME/KEY:
LOCATION:
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1411 TTTTAGTAGAATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAG 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Assons Matchias H.
APPLICANT: Assons Matchias H.
APPLICANT: Assonson, Stuart A.
TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
TITLE OF INVENTION: EPIDERAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND
WUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 400
STREET: 133 Carneqie Way, N W
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1.1%; Score 60; DB 1; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              join(66..221, 780..855, 1040..1185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/475,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/444,406
PILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: PELTYMEN, DAVIG G
REGISTRATION NUMBER: 31,438
REFRENCE/DOCKET NUMBER: 1414-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEPHONE: (404) 688-0770
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 1542 base pairs
TYPE: nucled acid
STRANDEDNESS: single
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COUNTY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; Patent No. 5916755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,895
FILING DATE:
                            exon
1040..1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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856..1039
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222..779
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LOCATION: 66..221
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LOCATION:
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US-08-473-119-1
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5453 TTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAG 5512
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Sequence 3, Application US/09749588

Patent No. 6423521

GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISWARAN, IShwar et al
TITLE OF INVEWITON: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVEWITON: THEREOF
FILE REFERENCE: CLOO1068
CURRENT APPLICATION NUMBER: US/09/749,588
CURRENT APPLICATION NUMBER: 2000-12-28
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 36159

"WINDER OF SEQ 150
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1.1%; Score 58; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e-13;
Matches 58; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 1.5e-13;
les 60; Conservative 0; Mismatches 0;
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; COTATION: (1)...(36159)
OTHER INFORMATION: n = A,T,C or G
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1040..1185
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856..1039
780..855
                    FEATURE:
NAME/KEY:
LOCATION:
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ORGANISM: Human
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LOCATION:
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LOCATION:
US-08-475-352-1
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US-09-749-588-3
                                                                                                                                                                                                                                                     FEATURE:
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008663 mus musculu
P38062 rattus norv
015488 homo sapien
Q9y2x3 homo sapien
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homo sapien
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macaca mula
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MEDLINE=91178815; Pubmed=1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quentin Y.;
"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Wol. Evol. 27:194-202(1988).
                       014628
Q13428
P53245
P36133
                                                                                                  P53908
P32633
P38808
P38808
Q48459
Q90kr8
P13825
P20042
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Q91375
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                                                                           Q921S5
P78563
 099959
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SC sequence contamination warning entry.
                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                              YK20_YEAST
SEP3_MOUSE
RED1_HUMAN
                                                                                                   YNO3_YEAST
YED3_YEAST
YHP5_YEAST
YC13_KLEPN
                                                                                                                                                     NKGC_MACMU
TM4B_HUMAN
ASP_PLAFS
             CRBA_DROME
2195_HUMAN
TCOF_HUMAN
YG2C_YEAST
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SX14_DROME
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AMP2_MOUSE
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GYG2_HUMAN
NOP5_HUMAN
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ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed-3138422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95021758; PubMed=7935834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92241891; PubMed-1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claverie J.-M., Makalowski W.;
"Alu alert.";
Nature 371:752-752(1994).
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 NCBI_TaxID=9606
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CONCEPT.
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ALUS_HUMAN
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6581.309 Million cell updates/sec
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1736
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                                                                                      ; Search time 69.5 Seconds
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P47152
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                              protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    112892 segs, 41476328 residues
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ALU8_HUMAN
ALU7_HUMAN
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ALU6_HUMAN
ALU4_HUMAN
ALU4_HUMAN
YJ85_YEAST
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ALU5_HUMAN
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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPES MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREEN POTENTIALY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GENSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH EL CONSQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                  MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPRANTE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
Homo sapiens (Human)
            585
16
0
          Length:
Matches:
Conservative:
Mismatches:
                                                         Indels:
                                                                                             US-09-966-880A-9 (1-5514) x ALU5_HUMAN (1-585)
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MEDLINE-95021758; Pubmed-7935834;
          9.09e-08
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Best Local Similarity:
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Alignment Scores:
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P39195;
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Length: Matches: Conservative:

9.08e-08 16.00 100.00%

Percent Similarity:

Score:

Claverie J.-M., Makalowski W.

Alignment Scores:

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THAT ALU REPEATS FALL INTO 8 SUBFANILIES: THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                         "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
                                                                                 MEDLINE-92241891; PubMed-1572661;
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANBOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Jurka J., Milosavljevic A.;
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"Alu alert.";
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P39195;
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SQ sequence contamination warning entry.
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BEDLINE-91178815; PubMed-1706781;
JUTKA J. Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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Claverie J.-M., Makalowski W.;
"Alu alert.";
Nature 371:752-752(1994).
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MEDLINE-88333009; PubMed-3138422;
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01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last anno
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ACID SEQUENCES.

-!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ALTO CAUTION: ALU REPETITIVE SEQUENCES SPACING OF 4 KB. SOME OF THEM ARE ALTO-DERIVED SEQUENCES IN 5' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN 5' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREWE ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS. ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE CLONIS ARTICLES AND OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH SET ALLY SERONDED OF SEQUENCING THE CONSEQUENCE OF MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF ERRONDEDUR ALU DERIVED AMINO ACID SEQUENCES
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                   MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                         MISCELLANDOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPRATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
14 Subfamily $0.5 sequence contamination warning entry.
15 Homo sapiens (Human).
16 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
17 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAME-2.
FRAME-3.
FRAME-4.
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ACID SEQUENCES.

C-1-CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACID SEQUENCES.
C-1-CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND ACID SETTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN COMPANIES ALGO CONTAIN PARTIAL AND/OR REARRANGED CDMAS.
C-1-CALL LIBRARIES ALGO CONTAIN PARTIAL AND/OR REARRANGED CDMAS.
C-1-CALD WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.
C-CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLVED FROM A DIATAL THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH PRIMAL SEPROMENCES.
C-CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCING.
THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                                                                                                                                                                                                    "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARN CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
                                                                                                                                                                                                                                                                                                                 Quentin Y.;
"The Alu family developed through successive waves closely connected with primate lineage history.";
[4] Wol. Evol. 27:194-202(1988).
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                                                           PubMed-7935834;
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FRAME-5.
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LINE-88333009; PubMed-3138422;
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                                                                         Claverie J.-M., Makalowski
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 NCBI_TaxID=9606;
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                                                                                                                                                                                    Claverie J.-M.,
                                                                                             "Alu alert.
                                                                                                                                                  CONCEPT
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                                                                                                                                                                                                                                     Quentin Y.;
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                                                                                                                                                                                                                                                                                                                             J. VITO1. 65:3259-3267(1991).
-!- FUNCTION: MIGHT PLAY A ROLE IN IMMORTALIZATION OF SV40-INFECTED CELLS. MIGHT BE THE CELLULAR COUNTERPART OF THE VIRAL E5 PROTEIN.
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: TO THE HUMAN PAPILLOMAVIRUS E5 PROTEIN.
                                                                                                                                                                                                                                                                                                   Wagner S., Cullman G., Knippers R.;
"The Q300 gene: a novel transcription unit induced in simian virus
40-infected and -transformed mouse cells.";
                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
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TISSUE-Kidney;
MEDLINE-91237845; PubMed-1851876;
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Q02722;
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ACID SEQUENCES.

CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERGE SPACING OF 4 KB. SOME OF THEM ARE PRIMATE GENOMES WITH AN AVERGE SPACING OF 4 KB. SOME OF THEM ARE ACITYELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALG. DENAYS HOMEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS. HOMEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORENTATION. ALTHOUGH ALU ELEMENTA (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Mol. Evol. 27:194-202(1988).
                                                                                                                                              Alu subfamily SC sequence contamination warning entry.
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
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MEDLINE-88333009; PubMed=3138422;
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                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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-1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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Ol-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
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Mismatches:
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FRAME-2.
FRAME-3.
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FRAME-5.
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MEDLINE-95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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MEDLINE-88333009; Pubmed-3138422;
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Hypothetical protein.
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Pred. No.:
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ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBBARRIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDMAS. LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALUGREN POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE CLONING ARTIFACT OR MAY BE DUE TO MISINFERPETED FROM A DATA THIS POINT HAS BEEN OVERLONGY. WITH CONSEQUENCE OF ERRONICES OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A DATA. THIS POINT HAS BEEN OVERLONED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE.
                                                                                                                                                                                    CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Homo sapiens (Human).
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FRAME-2.
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FRAME-5.
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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Best Local Similarity:
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P39189;
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474 SerAlaSerGlnSerAlaGlyIleThrGlyValSerHis 486

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-:- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPES MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSCRIPED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE REGULTED FROM A CLONING RATIFACT OR MAY BE DUE TO MISUITARPROPERATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOORED ON SEVERAL OCCASIONS, WITH CONSEQUENCE OF ERRONBOUS ALU-DERIVED AMINO ACID SEQUENCES
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-I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                        closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
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                                                  MEDLINE-88333009; PubMed-3138422;
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Genomics 12:838-841(1992)
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US-09-966-880A-9 (1-5514) x ALU2_HUMAN (1-587)

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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Mol. Evol. 27:194-202(1988).
                                                          01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
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"Identifying coding exons by similarity sea:
potentially misleading protein sequences.";
Genomics 12:838-841(1992).
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MEDLINE-95021758; Pubmed-7935834;
Claverie J.-M., Makalowski W.;
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Jurka J., Milosavljevic A.;
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  STANDARD;
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Jurka J., Milosavljevic A.;
Jurka J., Milosavljevic A.;
J. Molosavljevic A.;
J. Mol. 2001. 32.105-121(1991).
-1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES: THEREPECKE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Mol. Evol. 27:194-202(1988).
     Usage by
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
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modified and this statement is not removed. entities requires a license agreement (See ) or send an email to license@lsb-sib.ch).
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PERMATE GENOMES WITH AN AVERAGE SPACING OF 4 KE. SOME OF THEM ARE PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KE. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORWAL TRANSCRIPTS MAY CONTAIN ALL-DERIVED SEQUENCES IN 5' ON 3' UNTRANSCRIPTS MAY CONTAIN ALL-DERIVED SEQUENCE IN AND/OR RERRRANGED CDNAS LIBRARIES ALSO CONTAIN PARTIAL AND/OR REMRANGED CDNAS LIGATED WITH ALLU-DERIVED SEQUENCE IN AND ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN RADING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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Catarrhini; Hominidae; Homo.
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Claverie J.-M., Makalowski W.;
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Mammalia, Eutheria, Primates;
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Nature 371:752-752(1994).
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US-09-966-880A-9 (1-5514) x ALU1_HUMAN (1-591)

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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL FRANSCRIPTS MAY COMTAIN ALU-DERIVED BY POL III. NORMAL FRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CONAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
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                                                                                                        "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
"L. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEGUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE.
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Best Local Similarity:
Query Match:
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Alignment Scores:

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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIBETS MAY COMYAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GEREAT POTENTIAL. TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE NOT TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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Jurka J., Milosavljevic A.;
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J. Mol. Evol. 32:105-121(1991).
J. Mol. Evol. 32:105-121(1991).
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Mol. Evol. 27:194-202(1988).
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                              "Alu alert.",
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                                      ALU1_HUMAN
P39188;
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                     ALU1_HUMAN
RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALU FAMILIES CLASSIFICATION.

MEDLINE-91178815; PubMed-1706781;

Jurka J., Milosavljevic A.;

"Reconstruction and analysis of human Alu genes.";

J. Mol. Evol. 32.105-121(1991).

-I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potentially misleading exons by similarity search: alu-derived and other Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                665D395735519D95 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SP sequence contamination warning entry.
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Mismatches:
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FRAME-2.
FRAME-3.
FRAME-4.
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MEDLINE-95021758; Pubmed-7935834;
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MEDLINE-88333009; PubMed-3138422;
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"Alu alert.";
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P39193;
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                                                                                                                                             CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL. TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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                                                     MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP COODN, 'XXX' IS USED TO SEPRANTE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.
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P39193;
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-!- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACITYELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CONA INTERNATED REGIONS. HOWEVER, LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE REGULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
CONSENSUS SEQUENCES HARE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Genomics 12:838-841(1992).
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
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MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljevic A.;
MEDLINE-95021758; PubMed-7935834;
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MEDLINE-88333009; PubMed-3138422;
                              averie J.-M., Makalowski W.;
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or send an email to license@isb-sib.ch)

EMBL; U14572; -; NOT_ANNOTATED_CDS

Hypothetical protein. DOMAIN 1 9 136EF344AACD12A2 CRC64;

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FRAME-1. FRAME-2. FRAME-3. FRAME-4. FRAME-5.

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Alignment Scores:

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TISSUB-COLON MUCOSA;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayasai M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Nakamura Y., Isogai T., Sugano S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK000241; BAA910281; -.
InterPro; IPR001849; PH.
InterPro; IPR001869; SH2.
Pfam: PF00017; SH2.
SMART; SM00233; PH; I.
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Q9HAJ0
Q9H654
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NCBI_TaxID=9606;
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6844.240 Million cell updates/sec
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Compugen Ltd.

    protein search, using frame_plus_n2p model

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Copyright (c) 1993 - 2003
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sp_bacteriap:*
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Query Match:

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Q9D443

RESULT Q9D443

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Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
NCBI_TaxID=5664;
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                       Barrell
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Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
Gerrard C., Rajandream M.A., Barrell B.G.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL359782; CAB95454.1; --
SEQUENCE 188 AA; 20899 MW; 9EEABAD143A19071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Possible (hhv-6) ull02, variant a dna, complete virlon genome.
                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Probable (Hhv-6) ull02, variant a DNA, complete virion genome
                                                                                                                                                                                                                                                                                                                                                         D., Rajandream M., Ivens A., EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                          104 AA; 11240 MW;
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Submitted (JUL-2000) to the
EMBL; AL160493; CAB98117.1;
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
Rabata K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rabata K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rabata J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ruetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rayashizaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Rayashizaki V., V.
                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AKO16814; BAB3045.1; -. MGD; MGI:1922977; 4933415A048ik.
SEQUENCE 101 AA: 10943 MW; 0504048D1663D5EA CRC64;
                                     BCB572FEBD84BB83 CRC64;
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STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21055660; Pubmed-11217851;
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SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
SEQUENCE 449 AA; 49648 MW;
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Best Local Similarity:
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                                                                                                                         Percent Similarity
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01-JUN-2001
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STRAIN=U1102;
MEDLINE=92333248; PubMed=1321205;
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MEDLINE-92333249; PubMed-1321206;
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J. Virol. 66:1564-1570(1992).
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SEQUENCE FROM N.A.
           FROM N.A.
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Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W., Barrell B.G.; "Human herpesvirus 6 is closely related to human cytomegalovirus."; J. Virol. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-U102;
SPIRAIN-U102:
PUDMed=7747482;
Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Gompels U.A., Nicholas J., Lawrence G., Macaulay H.A.;
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
Martin M.B., Efstathiou S.,
The DNA sequence of Human Herpesvirus-6: structure, coding content,
and genome evolution.";
and genome evolution.";
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39 kDa antigen.
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Jing B., Hu X.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ CRC64;
EMBL; U83280; AAB47253.1; -.
SEQUENCE 322 AA; 34527 MW; 89F697DCB41B8959 CRC64;
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Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=10368;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE=91237802; Pubmed=1851860;
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MEDLINE=90080132; PubMed=2152817;
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ACCOSON REPARANCE REPARANC

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Thomson B.J., Honess R.W.;

"The right end of the unique region of the genome of human herpesvirus
"The right end of the unique region of the gene enhancer and a
6 U1102 contains a candidate immediate early gene enhancer and a
homologue of the human cytomegalovirus US22 gene family.";
J. Gen. Virol. 73:1649-1660(1992).
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Infectivity determinants encoded in a conserved gene block of human herpevirus-6.
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MEDLINE=91374590; PubMed=1654446;
MEDLINE=91374590; PubMed=1654446;
Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;
Indentification of a transactivating function mapping to the putative
immediate-early locus of human herpesvirus 6.";
J. Virol. 65:5381-5390(1991).
STRAIN-U1102;
MEDLINE-91333007; PubMed-1651403;
MEDLINE-91333007 Jones M.D.;
Teo I.A., Griffin B.E., Jones M.D.;
Teo I.A., Griffin of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
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MEDLINE-92148942; PubMed=1310766;
MEDLINE-92148942; PubMed=1310766;
MEDLINE-92148942; PubMed=1310766;
MEDLINE-92148942; PubMed=1310766;
MEDLINE-92148942; PubMed=1310766;
Meden V., Chandran B., Josephs S.F., Wood C.;
Identification and characterization of a human herpesyirus 6 gene 11dentification and characterization of a human immunodeficiency virus type 1 segment that transactivates the human immunodeficiency virus
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MEDLINE=92260671; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
Neipel F., Ellinger K., fleckenstein protein (p100) of human "Gene for the major antigenic structural protein (p100) human hernesyirus 6.";
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MEDLINE-91226542; PubMed-1851252;
Thomson B.J., of the human adeno-associated virus type-2 rep gene "Acquisition of the human adeno-associated virus type-6";
human herpesvirus type-6";
Nature 351:78-80(1991).
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MEDLINE-93389439; PubMed-8397282;
Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
Liu D.X., Gompels W.A., Nicholas J., Lelliott C.;
Identification and expression of the human herpesvirus 6 glycoprotein H and interaction with an accessory 40K glycoprotein.";
J. Gen. Virol. 74:1847-1857(1993).
                                               Gompels U.A., Carrigan D.R., Carss A.L., Arno J.; Two groups of human herpesvirus 6 identified by sequence analyses of laboratory strains and variants from Hodgkin's lymphoma and bone
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MEDLINE-93331710; PubMed-7687803;
Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton I Greenamoyer C., Dambaugh T.R.;
"A strongly immunoreactive virion protein of human Herpesvirus 6 variant B Strain Z29: identification and characterization of the ge and mapping of a variant-specific monoclonal antibody reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of a 21-kilobase-pair region of the genome of human herpesvirus containing homologues of human cytomegalovirus major immediate-early and replication genes."; submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                    MEDLINE-93224882; PubMed-8385692;
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                                                                                         marrow transplant patients.";
J. Gen. Virol. 74:613-622(1993).
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Virology 195:521-531(1993).
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Schiewe U., Neipel F., Schreiner D., Fleckenstein B.; "Structure and transcription of an immediate-early region in the human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Nucleotide sequence analysis of a 38.5-kilobase-pair region of genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions."; J. Virol. 68:597-610(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human cDNA clones with function of inhibiting cancer
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EMBL: AF258559; AAG23762.1; --
SEQUENCE 102 AA; 11514 MW; 9812289865490F91 CRC64;
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MEDLINE-94202284; Pubmed-8151768;
MEDLINE-94118404; PubMed-8289364;
                                                                                                                                                                                                           herpesvirus 6 genome.";
J. Virol. 68:2978-2985(1994).
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                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                  REAUTOLINE-STUBSEG, TISSUE-TESTIS;

RA MININ-C57BL/6J; TISSUE-TESTIS;

RA MININ-C57BL/6J; TISSUE-TESTIS;

RA MININ-C57BL/6J; TISSUE-TESTIS;

RA ALZAWA T., HATA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA ALZAWA T., Rand H., Kiyosawa H., Kondo S., Yamanaka I.,

RA ALZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA ALZAWA T., Astburner M., Batalov S., Casavant T.,

RA Galto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Galto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Galtin D., Lewis S., Marsuo Y., Nikaido I., Rochiwa H.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC012514; AAH12514.1; -.
SEQUENCE 535 AA; 58713 MW; 86E6DD3B545E96D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11866 MW; E5DD1919AC9B9ED2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to hypothetical protein.
                        Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-TESTIS, AND EMBRYONAL CARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us-09-966-880A-9 (1-5514) x Q9D324 (1-112)
  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL; AK016929; BAB30502.1; -.
MGD; MGI:1918322; 4933426F18R1k.
8.86e-08
17.00
100.00%
100.00%
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                                           (TrEMBLrel.
  (TrEMBLrel.
                          (TrEMBLrel.
                                                                 4933426F18R1k protein.
4933426F18RIK.
                                                                                                                  Mus musculus (Mouse).
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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Q96EB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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AC DE PAC DE PAC
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096EM6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:20106).
Unknown (protein for MGC:20106).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       5446 TTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTC 5496
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                         423 PheValPheLeuValGluMetGlyPheHisHisValGlyGlnAlaGlyLeu 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014203; AAH14203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC012108; AAH12108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
7CB5A2DDB7D79128 CRC64;
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16
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Conservative:
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Mismatches:
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                                                    Indels:
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                                                                      Gaps:
                                                                                                      US-09-966-880A-9 (1-5514) x Q96EB1 (1-535)
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                                                                                                                                                                                                                                                                              Created)
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01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
Hypothetical 5.3 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA; 5314 MW;
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16.00
100.00%
100.00%
0.92%
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16.00
100.00%
17.00
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0.98%
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us-09-966-880a-9.olin2p.rspt

Query Match:

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US-09-966-880A-9 (1-5514) x Q96AN9 (1-73)
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Q9H654
                                                                                                                                                       09HAJ0
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Hypothetical (TrEMBLrel. 19, Last annotation update)
Hypothetical (B kna protein.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
WCBL_TaxID=9606; Homo.
                                                                      Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheries; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausbarg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016905; AAH16905.1; -.
Hypothetical protein.
SEQUENCE 73 AA; 8348 MW; 673F61E85300AC2F CRC64;
           00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452AB9CAB00ADC3D CRC64;
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16
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01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
similar to hypothetical protein PRO1722
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16
0
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Matches:
Conservative:
Mismatches:
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Matches:
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Mismatches:
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Gaps:
                            US-09-966-880A-9 (1-5514) x Q96EM6 (1-50)
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                                                                                                                                                                                                                                                                                                                                                                                             Strausborg R.;
Submitted (JAN-2001) to the EM EMEL; BC001672; AAH01672.1;
Hypothetical protein.
SEQUENCE 61 AA; 6835 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.07e-06
16.00
100.00%
100.00%
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16.00
100.008
100.008
0.928
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Best Local Similarity:
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TISSUE-BREAST;
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Best Local Similarity:
Query Match:
DB:
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Pred. No .
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Query Match:
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096AN9
1D 096AN9
AC 096AN6
DT 01-DEC
DT 01-DEC
DE SIMILE
OS HOMO &
CC EURALY
OX NCBLL
RP SEQUEN
RC TISSUE
RC TISSUE
RL SUDMILL
NR STEAUS
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A TISSUPE-EMBRYO:

RA Inshikawa T., Nagai K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Inshikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Takahashi M., Chiba Y. Ishida S., Murakwa K., Ono Y., Takiguchi S.,

RA Matanabe S., Kimura K., Murakmi K., Ishili S., Kawai Y., Saito K.,

RA Ninomiya K., Iwayanagi T.,

RT "MEDO human cDNA sequencing project.",

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

Sequence 121 AA, 13691 MW; 265372CF6CBFE856 CRC64;
                                                                                                                                    09HAJO;

01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-0CT-2001 (TrEMBLrel. 18, Last annotation update)

Hypothetical 13.7 kDa protein.

Hypothetical 13.7 kDa protein.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01.MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ22596 (Is, clone HSI03808.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. SEQUENCE FROM N.A.

*C TISSUE-SMALL INTESTINE;

RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota
RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,

*Namura Y., Isogai T., Sugano S.;

*NEDO human cDNA sequencing project.";

RL Subnitted (AuG-2000) to the BMBL/GenBank/DDBJ databases.

SQ SEQUENCE 160 AA; 16738 MM; FBBB34293C8E27E7 CRC64;
                      52 CysilePheSerArgAspGlyValSerProCysTrpProGlyTrpSer 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5448 TGTATTTTAGTAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCT
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16
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Conservative:
Mismatches:
Indels:
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Matches:
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16.00
100.008
100.008
0.928
                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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0000 Conservative: Mismatches: Indels: Gaps: Percent Similarity: 100.00% Best Local Similarity: 100.00% Query Match: 4

US-09-966-880A-9 (1-5514) x Q9H654 (1-160)

ò qq Search completed: June 14, 2003, 19:30:13 Job time : 350 secs

		
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538, App 131, App 131, App 131, App 121, App 121, App 2, Appl 2, Appl 131, Appl 121, Appl 122, Appl 123, Appl 124, Appl 125, Appl 127, Appl 127, Appl 127, Appl 127, Appl 128, Appl 129, Appl 121, Appl 121, Appl 121, Appl 121, Appl 122, Appl 133, Appl 134, Appl 135, Appl 137, Appl 137, Appl 138, Appl 139, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 137, Appl 138, Appl 139, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 137, Appl 138, Appl 139, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 137, Appl 138, Appl 139, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 137, Appl 138, Appl 139, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 137, Appl 138, Appl 138, Appl 139, Appl 131, Appl 131, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 136, Appl 137, Appl 138, Appl 138, Appl 139, Appl 130, Appl 131, Appl 131, Appl 131, Appl 132, Appl 133, Appl 134, Appl 135, Appl 136, Appl 137, Appl 138, Appl

Title: Perfect score:

Sequence:

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Minimum DB Maximum DB

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US-09-439-313-538

US-09-227-357-538

US-09-227-357-171

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US-09-227-357-171

US-09-227-357-171

US-09-227-357-171

US-09-025-371-11A-121

US-09-025-375-537

US-09-065-946-22

US-09-465-970-2

US-09-465-970-2

US-09-288-143-170

US-09-288-143-170

US-08-449-741-13

US-08-449-741-13

US-08-449-741-13

US-08-449-741-13

US-08-449-754-13

US-09-288-143-93

US-09-288-143-93

US-09-465-646-12

US-09-288-143-93

US-09-288-143-93

US-09-288-143-93

US-09-288-143-93

US-09-288-143-93

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US-09-288-143-93

US-09-288-143-93
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TITLE OF INVENTION: 123 Human Secreted Proteins
TITLE OF INVENTION: 123 Human Secreted Proteins
CURRENT FILING 12910P1
CURRENT FILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER PRILING DATE: 1997-07-08
EARLIER PRILING DATE: 1997-07-08
EARLIER PRILING DATE: 1997-07-08
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US-09-265-630-11
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Patent No. 6342581
GENERAL INFORMATION:
    US-09-227-357-171
      0000000000
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7, Appli
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                                                                                                                                                           (without alignments)
6180.495 Million cell updates/sec
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1736
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                protein search, using frame_plus_n2p model
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US-09-605-786-825
US-08-454-557C-121
US-08-450-673C-121
US-08-153-484-7
US-09-088-337B-7
US-09-088-337B-7
US-09-088-337B-7
US-09-088-337B-7
US-09-088-337B-7
US-09-088-337B-7
US-09-088-337B-7
US-09-605-785-538
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seq length: 200000000
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Sequence S

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Result 8 υ

Database

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Mitcham, Jennifer L.

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Matches:
Conservative:
Mismatches:
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EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-09-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-09-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-09-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER APPLICATION NUMBER: 60/05
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 90
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US-09-605-785-827
Sequence 827, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

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GENERAL INFUGANT:

GENERAL INFUGANT:

APPLICANT:

APPL
                                                                                                                                                                                                                                                                     APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DAGE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5462 AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC 5503
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Matches:
Conservative:
Mismatches:
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                                      Fanger, Gary R. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick Li, Samuel
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100.00%
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; ORGANISM: Homo sapiens
US-09-605-785-827
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Best Local Similarity:
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LENGTH: 96
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APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: Of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                    APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3605 TCAGCCTCCCAGAGTGCTGGGATTACAGGCGTGAGCCACCAC 3564
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                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
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14
0
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                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 128 PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                          ; Sequence 121, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
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; Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R.
REGISTRATION UNDRER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                          Washington
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                       CITY: Wash
STATE: D.C
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                         US-08-340-426D-121
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Sequence 121, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Allzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         5462 AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC 5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3605 TCAGCCTCCCAGAGTGCTGGGATTACAGGCGTGAGCCACCAC 3564
                                                                                                                                                                                                                                                                                                                  211 ArgTrpGlyPheThrMetLeuAlaArgLeuValSerAsnSer 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-MAY 1995
CLASSIFICATION: 514
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCETOROKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEG ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                        Indels:
                                                                                                0.000118
14.00
100.008
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-605-785-825
                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                 Alignment Scores:
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Patent No. 5759804
GENERAL INFORMATION.
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3605 TCAGCCTCCCAGAGTGCTGGGATTACAGGCGTGAGCCACCAC 3564
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FLING DATE: 30-MAY-1995
CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-260
INFORMATION FSQ 10 NO: 121:
ELENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-673C-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Blcknell
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-966-880A-9 (1-5514) x US-08-450-673C-121 (1-375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0507/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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STATE: Illinoi
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STREET: 630
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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            3291 ATGATTGCACCACTGCACTCCAGCCTGGGTAACAGGGTGAGA 3250
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-966-880A-9 (1-5514) x US-08-153-848-7 (1-410)
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REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UNN-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01/977,452
FILING DATE: 17-NOV-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09299843A Patent No. 6107475
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
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TELEFAX: (312) 474-0448
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                                                                                                                                                   ; MOLECULE TYPE: protein US-08-153-848-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sear CITY: Chicago STATE: Illinois COUNTRY: USA
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                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
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                                                                                                      RESULT 10
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC Compatible

COMPUTER: IEM PC COMPATIBLE

CURRENT APPLICATION DATA:

CLASSIFICATION NUMBER: US 09/088,337B

FILING DATE: 01-Jun-1998

CLASSIFICATION NUMBER: US 08/153,848

APPLICATION NUMBER: US 08/153,848

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

FILING DATE: 17-NOV-1993

FILING DA
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-3378-7
                                                                                                                                                                                                 Gaps:
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STATE: Illinois
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Best Local Similarity:
Query Match:
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, MOLECULE TYPE: protein US-09-299-843A-7
                                                                                                                               Percent Similarity: 1
Best Local Similarity: 1
Query Match: 3
DB:
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pred. No.:
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                                                                              Alignment Scores:
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RESULT 11
US-09-058-489-22
Sequence 22, Application US/09058489
Sequence 22, Application US/09058489
Patent No. 6103886
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application PC/TUS9311153
Sequence 7, Application PC/TUS9311153
GENERAL INFORMATION: Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Vic
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STREET: 6300 Sears Tower, 233 South Wacker Drive
STREET: 6300 Sears Tower, 233 South Wacker Drive
CTTY: Chicago
STATE: 111hous
COUNTRY: USA
ZIP: 66666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PROPENSE PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0,
APPLICATION NUMBER: PCT/US93/11153
APPLICATION NUMBER: PCT/US93/11153
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Mismatches:
Indels:
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US-09-966-880A-9 (1-5514) x US-09-088-337B-7 (1-410)
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CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION UNBER:
APPLICATION UNBER:
FILLING DATE:
17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME:
NAME:
NAME:
NAME:
NAME:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX:
TELEFAX:
1312) 474-6300
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INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH:
ATTOR
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US-09-966-880A-9 (1-5514) x US-09-605-785-538 (1-1261)
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Best Local Similarity:
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APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHIST-OBPA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
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US-09-605-785-538
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LENGTH: 1079
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LENGTH: 1261
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 201021 427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 538
LENGTH: 1261
TYPE: PRI
5462 AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCC 5503
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APPLICANT: Fischer et al.
TILLE OF INVENTION: 123 Human Secreted Proteins
FILLE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
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EARLIER FILLIG DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILLING DATE: 1997-07-08
                                                                                                                                                  Sequence 538, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
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                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                 APPLICANT: MILL...

APPLICANT: Harlocker, sur...

APPLICANT: Jiang Yuqui

APPLICANT: Reed, Steven G.

APPLICANT: Renger, Michael

APPLICANT: Ranger, Gary

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Solk, John

APPLICANT: Solk, John

TANT: Day, Craig
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US-09-439-313-538
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RESULT 15
US-09-184-930-131
US-09-188-930-131, Application US/09188930A
Sequence 131, Application US/09188930A
Sequence 131, Application US/09188930A
Sequence 131, Application US/09188930A
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: 1000 L010.10
CURRENT FILING DATE: 1998-11-09

			Length: 65 Matches: 13 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0 Gaps: 1-65) GCTGAGGTGGTGGA 3615 [
APPLICATION NUMBER: 60/051,931 PFILING DATE: 1997-07-08 APPLICATION NUMBER: 60/051,932 APPLICATION NUMBER: 60/051,916 APPLICATION NUMBER: 60/051,916 FILING DATE: 1997-07-08	PPLICATION NUMBER: ILING DATE: 1997-0 ILING DATE: 1997-0 ILING DATE: 1997-0 ILING DATE: 1997-0 PPLICATION NUMBER: PPLICATION NUMBER: PPLICATION NUMBER: PRILING DATE: 1997-0 PPLILING DATE: 1997	1997-08 NUMBER: 1997-08 NUMBER: 1997-07 1997-09 1997-09 1997-0 1997-0 1997-0 10WBER: 1997-0 1 NUMBER: 1997-0 2 1997-0 2 1997-0 2 1997-0 3 1997-0 3 1997-0 5 1997-0 5 1997-0 5 1997-0 5 1997-0 5 1997-0	Alignment Scores: 0.00118 Length: Pred. No.: 13.00 Conservative: 13.00 Conservative: 100.00\$ Mismatches: 100.00\$ Mismatches: Best Local Similarity: 100.00\$ Indels: 0.75% Gaps: 108-09-966-880A-9 (1-5514) x US-09-227-357-538 (1-65) US-09-966-880A-9 (1-5514) x US-09-227-357-538 (1-65)

Search completed: June 14, 2003, 19:37:45 Job time: 90.5 secs

US-09-966-880A-9 (1-5514) x US-09-188-930-131 (1-70)

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Mismatches:
Indels:
Gaps:

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Alignment Scores:

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S. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987. DAT:

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S. SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999. DAT:

S. SIDS2/gcgdata/geneseq/geneseqn-embl/NA20018. DAT:

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Copyright (c) 1993 - 2003
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Human proto-oncoge Genomic sequence # Genomic sequence # Human cDNA differe Human immune/haema Human reproductive Human testicular a

Oesophagus cancer Genomic sequence # Human musculoskele

AAK67239
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ABA15431
ABA15431
ABC68207
ABC68117
ABA96614
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ABK62218
ABK62218
ABK62218
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Human activation-i	Human activation-i	Human activation-i	Human activation-i	Human immune/haema	Mouse activation-i	Human immune/haema	Human immune/haema	O
SUMMARIES			Y	AAC55312W	AAC55314	AAC55339	AAC55319	AAK81088	AAC55307	AAK81089	AAK61819	ABA08208
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Human immune/haema						Human activation-induced cytidine deaminase encoding cDNA SEQ ID NO:7.		Activation-induced cytidine deaminase; AID; cytidine deaminase;	immune related disease; allergy; allergic disease; antiallergic;	antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;	gene therapy; B cell associated immune system disorder; food allergy;	immunodeficiency disease; immunoglobulin A deficiency disease; asthma;	IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;	sase; DiGeorge disease; AIDS;	ataxia telangiectasia; common variable immunodeficiency disorder;	y disease;	ss selection disorder; ss.					"activation-induced cytidine deaminase"				
22 AAK67239	ALIGNMENTS	9	2818 BP.			cytidine deaminase	•	ne deaminase; AID;	llergy; allergic d	c; ophthalmologica	clated immune syst	immunoglobulin A	ulinaemia; atopic	initis; Rosen dise	nmon variable immu	<pre>major histocompatibility class II deficiency disease;</pre>	auto immunodeficiency syndrome; IgG subclass		Location Zonalifiers			"activation-induc				
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GACCCCAAACCATCTCTCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAG
  CTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGT
                                                                                             TACTTTGGGACTTTGATAGCAACTTCCAGGAATGTCACACACGATGAAATATCTCTGCTG
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(AID) AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallargic,
antianaemic, antiasthmatic, ophthalmological, anti-HYV and
dermatological activities, and can be used in gene therapy. AID
collinucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunoglobulin A (19A) deficiency
clisease, igh nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, DiGeorge disease, ataxia telangiectasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
ig disorder, and igg subclass selection disorder. The DNA sequences
encoding AID may be used for gene therapy and the antibodies to the AID
encoding AID may be used for gene therapy and the antibodies control
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                                                                                                                                                                                         useful
                                                                                                                                                                               Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein may be used for diagnosis and treatment of these disorders
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100.0%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                                                                           Claim 3; Page 135-139; 174pp; Japanese.
                         99JP-0087192.
99JP-0178999.
99JP-0371382.
28-MAR-2000; 2000WO-JP01918
                                                                              (NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
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Matches 2818; Conservative
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P-PSDB; AAB24198.
                                       24-JUN-1999;
27-DEC-1999;
                          29-MAR-1999;
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CC colitis, astmma, rood allergy, drug allerg CC disease, DiGeorge disease, ataxia telangie CC immunodeficiency disorder, MHC (major hist CC II deficiency disease, ADS (auto immunode CC IgE disorder, and IgG subclass selection de		2581 GTAATTGTAACATTGCAGTAATGGTGCTACGAAGCCATTTCTCTTGATTTTTAGTAAACT 2640
		2521 AATGGAGTCTCAAAAGCTTCATAAATTTATAACTTTAGAAATGATTCTAATAACAACGTAT 2580
has cytidine activity similar transcensic, antianaemic, antiasthmatic, opht dermatological activities, and committees, and contrological activities, and		2461 TTATATTATTGCGTCTAATGATTTTTATTAACATGATTTCCTTTTCTGATATTGA 2520
	. a × 0 0	2401 TTATTGTACATAAGTTTGTAAAAGAGTTAAAAATTGTTACTTCATGTATTCATTTATATT 2460
PT Nucleic acid encoding activation induced c PT a target for drug development for immune-r. PT allergies		2341 TGCAATGAAGATGAGCAGAAAACTTGAATGCACAACTGTCTTATTTAATC 2400
WPI; 2000-611715/58.	<u>× </u>	
XX PI Honjo T, Muramatsu M;	× 0	2281 GACAGTGAGAAAAATATTCAGAATAACCATATCCCTGTGCCGTTATTACCTAGCAACCT 2340
(NISB) JAPAN TOBACCO INC. (HONJ/) HONJO T.		2221 GCCAATAAGGGATCCCTATTTGTCTCTTTTGGTGTCTATTTGTCCCTAACAACTGTCTT 2280
XX XX PR 29-MAR-1999; 99JP-0087192. PR 24-UUN-1999; 99JP-018999. PR 27-FRC-1900.		2161 GGAGAGAAGGATGGGAAGCATTGCAAGGAAATTGTGCTTTATCCAACAAATGTAAGGA 2220
05-OCT-2000.	- × a ×	2101 AGACTCTGTCTCAGAAAAAAAAAAAAAAAGAGAGAGAGAG
XX		2041 GGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCGAGCTGGGGGACAAGAGCA 2100
KW drug allergy; allergic rhinitis; Rosen diu KW drug allergy; allergic rommon variable im KW mataxia telangiectasia; common variable im KW major histocompatibility class II deficie		1981 AGGCACCTGFAATCCCAGCTACTTGGGAGGCTGAGGCAGAGAATCGCTTGAACCCAGGA 2040
KW antianeemic; antiasthmatic; ophthalmologic KW antianeemic; antiasthmatic; ophthalmologic KW gene therapy; B cell associated immune sys KW immunodeficiency disease; immunodejlobulin A		1921 GGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGC 1980
Ax Ax Human activation induced cytidine deaminas XX XX Activation induced cytidine deaminase; AID XV in immination induced cytidine deaminase; AID		1861 CAGCACTTTGGGAGCCGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCT 1920
XX XX AAC55314; XX XX	· « × ۵ ›	1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
RESULT 2 AAC55314 ID AAC55314 standard; DNA; 6564 BP.	∝ d ii ×	1741 TGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCAA 1800
Oy 2761 TAAATAAAAATCAGTATGATGGATAAACTT 	~ ^	1681 AGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCGAGGTTGAGGAGGAGGAGGAGA 1740
2701	<u> </u>	1621 GATGCTTCTCCCAAAGGTATATTAACTATATAAGAGTTGTGACAAAACAGAATGATAA 1680
Qy 2641 TTTATGACAGCAAATTTGCTTCTGGCTCACTTT	<u> </u>	1561 GGGTCTCTTCATCTCAGAATGCCAATCAGGTCAAGGTTTGCTACATTTTGTATGTGTGT 1620

AAATAATATAAAAGTGATTTATATGAAGT 2760 AID; cytidine deaminase; gic disease; antiallergic; ggical; anti-HIV; dermatological; system disorder; food allergy; in A deficiency disease; asthma; ppic dermatitis; allergic colitis; disease; Diceorge disease; AIDS; immunodeficiency disorder; ichency disease; oclass selection disorder; ds. The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantamic, ophthalmological, antiallergic, antiathmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency disease and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences cytidine deaminase, useful as related diseases including se genomic DNA SEQ ID NO:10. ပ္ပ

TATTICICICITITGGIGICTATITGICCCTAACAACTGICTITGACAGIGAGAAAATA AGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTA ACTACTTGGGAGGTTGCAGGAGGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTA CTAATGATTTTTTATTAACATGATTTCTTTTCTGATATATTGAAATGGAGTCTCAAAGC CGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAA <u>AAAAAAAAAAAAAGAGAGAGAGAGAGAAAAGAGAACAATATTTGGGAGAGAAGGATGGGG</u> TTCAGAATAACCATATCCCTGTGCCGTTATTACCTAGCAACCCTTGCAATGAAGATGAGC <u> AAGAAAGAGAGAGGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC</u> **AAGCATTGCAAGGAAATTGTGCTTTATCCAACAAAATGTAAGGAGCCAATAAGGGATCCC** TTCATAAATTTATAACTTTAGAAATGATTCTAATAACAACGTATGTAATTGTAACATTGC AGTAATGGTGCTACGAAGCCATTTCTCTTTGATTTTTAGTAAACTTTTATGACAGCAAATT q à q δ q οy 9 9 9 0 0 0 90 90 ò Db Qy Q οy Dp ογ QQ οy g δ Q ò Db ò Db a ó

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The present invention describes an activation-induced cytidine deaminase
(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antialergic,
antiandemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
polynucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunoglobulin A (IgA) deficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhintis, Rosen
disease, bideorge disease, ataxia telangiectessia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
Ig disorder, and IgG subclass selection disorder. The DNA sequences
2716
                                   5834
                                                                   2776
                                                                                     Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianamenic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodefichency disease; immunodiobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; duty allergy; allergic rohintis; Rosen disease; biGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                   ATAAAATACCAAATAAAATAATATATAAAAGTGATTTATATGAAGTTAAAATAAAAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 163-170; 174pp; Japanese.
                                                                                                                                                      5895 TATGATGGAATAAACTTGAGA 5915
                                                                                                                                      TATGATGGAATAAACTTGAAA 2797
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24-JUN-1999;
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encoding AID may be used for gene therapy and the antibodies to the protein may be used for diagnosis and treatment of these disorders. present sequence represents a genomic DNA sequence of human AID.
                                                                    DB 21; Length 11204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergy allergic disease; antiallergic; antiantimatic; ophthalmological; antiintly; dermatological; gene therapy; B cell associated immune system disorder; food allergy; munnodeficiency disease; asthma; IgA nephritis; gamma-globulin A deficiency disease; asthma; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telandiscrasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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cytostatic; gene therapy; vaccine; metastasis; ds.
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of heamatopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic-derived cells. AAK64703
sequences from the present invention. AAK54951 contigen genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent sequences used in the exemplification of the present invention.
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Pred. No. 2.4e-238;
0; Mismatches 3;
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99.8%;
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polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinnemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhintis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IGE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                       GAAGCAGCCTTGCTTGAAGCAAGCTTCCTTTGGCCCTAAGACTTTGAGGAGTCAAGAAAG
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                                                                                                                                                                                                                                     Score 603.4; DB 21; Length 2440;
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Activation-induced cytidine deaminase; AID; cytidine deaminase; Immune related disease; allergy; allergic disease; antiallergic; antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telanglectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IGG subclass selection disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantamentc, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID
                                                CCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATCCC
                                                                   AGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTA
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93..689
7*tage a /*tage a /product activation-induced cytidine deaminase"
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           AATAGAGAAGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGC 902
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                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                         844 AGGACCGCCAGAGCAATGATGTAAC----
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proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to o prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers from the present invention. AAK6492 to AAK875950 and AAM82169 represent sequences from the present invention.
                                                                                                                                                                          Sequence 574 BP; 201 A; 80 C; 85 G; 208 T; 0 other;
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Matches 574; Conservative
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                                         Gaps
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0
            Length 574;
                                         Indels
          Score 574; DB 22;
Pred. No. 1.6e-86;
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20.4%; Scc.
100.0%; Pred
0; M
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2000US-0234998

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25 - SEP - 2000;
27 - SEP - 2000;
29 - SEP - 2000;
20 - CCT - 2000;
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17-NOV-2000;
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11-DEC-2000;
05-JAN-2001;
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 cytostatic; gene therapy; vaccine; metastasis; ss
                                                                                                                                 20000US - 0.18 664.
2000US - 0.18 664.
2000US - 0.18 664.
2000US - 0.18 664.
2000US - 0.20 6512.
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2000US - 0.20 664.
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2000US-0234274.
2000US-0234997.
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26 - JUL - 2000;
14 - AUG - 2000;
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14-SEP-2000;
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14-SEP-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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- MAR-2000;
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- APR-2000;
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                         Homo sapiens
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20000S - 0225834 20000S - 0225835 20000S - 0225836 20000S - 0225836 20000S - 0225836 20000S - 0225836 20000S - 0236369 20000S - 0241786 20000S - 0241809 20000S - 0241809 20000S - 0241809 20000S - 0241809 20000S - 0246474 20000S - 0246474 20000S - 0246526 20000S - 0246527 20000S - 0246619 20000S - 0246528 20000S - 0246529 20000S - 0249219 20000S - 024929 20000S - 025929 2000S - 025929 20000S - 025929 2000S - 025929 200S - 025929 2000S - 025929 2000S - 025929 2000S - 02592

20000S-0251989. 2000US-0251990. 2000US-0254097. 2001US-0259678.

AAK54951

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antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacteria!; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                              Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003
                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
ABA08208 standard; DNA; 13862 BP
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2000US-0224519.
2000US-0225213.
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2000US-0225759.
2000US-0226279.
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2000US-0232081
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22 - AUG - 2000)
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26-JUL-2000;
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01-SEP-2000;
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                                 ABA08208;
 and sequences given in AMM8170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87644 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK5450 and AAM82169 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAACCGTGGCACACGCTCATAGTTCTAGCTGCGTTGGGAGGTTGAGGAGGAGGATGGCT 1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                         to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                                                                                                                                                         Claim 1; SEQ ID NO 6879; 3071pp + Sequence Listing; English.
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                                             Ruben SM;
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             (HUMA-) HUMAN GENOME SCI INC.
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                                             Barash SC,
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P-PSDB; AAM89038.
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2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0234998.
2000US-0235484.
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2000US-0246609.
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        2000US-0232397
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2000US-0234223
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08-NOV-2000;
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02-0CT-2000;
02-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
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1727 TTGAGGAGGAGGATGCCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAG 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleic acids, proteins, antibodies and (antibodies are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes (ABA07454-ABA08224) and proteins (AABA0743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCTGTACTCAAAATTA
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01-DEC-2000, 2000US-0250391.
05-DEC-2000, 2000US-0251030.
05-DEC-2000, 2000US-0251988.
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08-DEC-2000, 2000US-0251866.
08-DEC-2000, 2000US-0251866.
08-DEC-2000, 2000US-0251869.
08-DEC-2000, 2000US-0251869.
08-DEC-2000, 2000US-0251999.
08-DEC-2000, 2000US-0251990.
11-DEC-2000; 2000US-0251990.
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GTTCAAGACCAGCCTGGACAACATGGCAAAACCCTGTCTCTATTAAAAATACAAAATTA 1807

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20000S-0229509
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20000S-0230438
20000S-0231242
20000S-0231244
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20000S-0231244
20000S-0232080
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 CGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCC 2085
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                                                                             2146 AGAGAACAATATTTGGGAGAAGGATGGGGAAGCATTGCAAGGAAATTGTG 2197
                                                                                        Human reproductive system related antigen DNA SEQ ID NO: 5477.
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Human; reproductive system related antigen; reproductive system disorder;
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              2146 AGAGAACAATATTTGGGAGAGAGATGGGGGAAGCATTGCAAGGAAATTGTG 2197
                                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 10204.
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  1868 CGTTTGAAGCCAGGAGGCGGAGTTTGCACCGAGAGTGTGCCCACTGCACTCCAGCC 1927
                                      immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic, cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucler; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                             2146 AGAGAACAATATTTGGGAGAGAAGGATGGGGAAGCATTGCAAGGAAATTGTG 2197
                                                                                                                                                                                            Human nervous system related polynucleotide SEQ ID NO 8055.
                                                                                                                                   ABA15724 standard; DNA; 7809 BP
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                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                              1252 TCACACCTGTAATCCCAGAACTTTGGGAGGCCGAGGTGGGCGGGATCACCTGAGGTCGAGG
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1726 GTTGAGGAGGAGGATGCCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAA 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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Pred. No. 9.6e-40;
0; Mismatches 104; Indels 10;
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Local Similarity 77.2%;
hes 385; Conservative (
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anthon acid sequences given in AAMB1921. (I) have cytostatic anthon acid sequences given in AAMB1921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) to proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally. (I) c supplement the patients own produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polynucleotides may be used to prevent.

C protein. (I) proteins and polynucleotides may be used to prevent.

diagnose and treat immune/haematopoietic-related diseases, especially cancer metastases of haematopoietic-derived cells. AAK64703

to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK849421 to AAK84950 and AAM82169

represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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           2000US-0246528
2000US-0246528
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2000US-0246610
2000US-0246611
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2000US-0249300.
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2000US-0251988.
2000US-025719.
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Sequence 30393 BP; 8271 A; 7315 C; 8076 G; 6731 T; 0 other;

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(HUMA-) HUMAN GENOME SCI INC

SM Rosen CA, Barash SC,

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system useful for preventing, cancers and metastases

Disclosure; SEQ ID NO 7762; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18011) useful for preventing, treating or ameliorating medical conditions e.g. by protein or the rapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone

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marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                            2040 AGGIGGAGGTIGCAGIAAGCIGAGAICGIGCCGTIGCACICCAGCCIGGGCGACAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1980 CAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG
                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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"I (bases 1 to 856)

"Ii, W. B., Gruber, C., Jessee, J. and Polayes, D.

"Full-length cDNA libraries and normalization

"In (bublished (2001)

"Contact: Genoscope

Genoscope - Centre National de Sequencage

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                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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26.2
25.0
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850.6 847 809.4 799.2 739.4

Score

Result . 8

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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8311 mmill: filiang@lifetech.com URL: http://fulllength.invitrogen.com 2 others
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                                                                                                                          Length 856;
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llarity 99.6%; Pred. No. 2.3e-90;
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/organism="Homo saplens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4853069"
/clone="IMAGE:4853069"
/clone="IMAGE:4853069"
/clone="Lub="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; vector: porB7; Site_1: xho1;
Site_2: Ecors: cons made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: aGGACGAGG(0: Size-selected >S00bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                  BG758510 872 bp mRNA linear EST 15-MAY-2001 602712721F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853069 5',
                                                                                                                                                                                                                                                                                                             E I (bases 1 to 872)

S NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1698 row: i column: 06

High quality Sequence stop: 836.
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99.38;
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/note="Organ: lymph, Vector: poTB7; Site_1: XhoI; Site_2: ECORI, CONA made by oligo-dT priming. Directionally cloned into ECORI, CONA made by oligo-dT priming. Directionally cloned into ECORI, Size-selected >500bp for average insert size of GecaGGG(G). Size-selected by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript Lin TR (Life Technologies). Note: this is a NIH_MGC and 236 c 233 g 246 t.
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            /clone="IMAGE:5929977"
/clone=lib="NH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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No. 1.3e-85;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 953)
1 (hases 1 to 953)
1 (hases 1 to 953)
Nath-Moc http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                     AAACAGTCCTTCAAGTCTTCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTAC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2108 row: p column: 10
High quality sequence stop: 634.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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       /db_xref="taxon:9606"
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/clone="IMAGE:476624"
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/tlssue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phag
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/organism="Homo/db_xref="taxon:
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BG/5/089 820 bp mRNA linear EST 15-MAY-2001
602715124F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855517 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGG
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                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
1 MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Clone distribution: MGC clone distribution information can
clone distribution: MGC clone distribution at:
http://image.llnl.gov
Plate: LLCMIT04 row: o column: 06
High quality sequence stop: 675.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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Pred. No. 1.7e-73;
0; Mismatches 24;
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/organism="Homo sapiens"
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BG757089.1 GI:14067742
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602245679F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4336722 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hong in the laboratory of Gerald M. Rubin (University or California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAGAAGGTAGATCCTAAAAAGCATGGTGAGAGGATCAAATGTTTTTATATCAACATCC
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                                                                                                                                                                    634 GGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGATAGCAACTTCCAGGAAT
                                                                                                                                                                                    GTCACACACGATGAAATATCTCTGCTGAAGACAGTGGATAAAAAACAGTCCTTCAAGTCT
                                                                                                                                                                                                                                               TCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTACAGAAAAAATTTATATA
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                                                                                                                                      7;
                                                                                                        Length 820
                                                                                                                                        Indels
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                                                                                                            DB 12;
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Pred. No. 1.9e-73;
); Mismatches 38;
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0
                                                                                                       25.0%;
llarity 94.5%;
Conservative (
                                                                                                                        Best Local Similarity
Matches 775; Conserv
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/organism="Homo sapiens"
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/db_arsn="Homo sapiens"
/db_arsn="Homo sapiens"
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-df priming:
Directionally cloned into EcoRi/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
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Homo sapiens cDNA clone IMAGE:4856568 5',
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CTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGT 360
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                       CCATGAAAGAACTTTCAAAGCCTGGGAAGGCTGCATGAAAATTCAGTTCGTCTCTCCAG
               GCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAA
                                                                                                                                                                                               GGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI707 row: k column: 01
High quality sequence stop: 638.
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BG755526.1 GI:14066179
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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1113

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753

693

Gaps

9

180

813

240

933 300 993 360

873

1173

540

1233

900

1293

099

1348

720

FEATURES

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/lab_host="brimary B-cells from tonsils (cell line)"
/lab_host="brimary B-cells from tonsils (cell line)"
/lab_host="brimary B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGGGG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, BerKeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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El (Dassi I to 942)

I (Dassi I to 942)

L Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution at the library Preparation of Consortium/LLNL at:

High quality sequence stop: 707.

Location/Qualifiers
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602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
                      ACAGTGGATAAAAAAACAGTCCTTCAAGTCTTCTCTGTTTTTTATTCTTCAACTCTCACTTT
                                          ATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCA
                                                                                                                                                                                               ACATTGTCCCCTACTGGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAA
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Pred. No. 4.1e-69;
0; Mismatches 61
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/organism="Homo sapiens"
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ilarity 91.3%;
Conservative
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BF975166
BF975166.1 GI:
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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11 (bases 1 to 693)
12 (bate) (base 1 tri, //mgc.nci.nih.gov/. Nathomal Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_48"
/tissue_lype="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                             Email: capbs_remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Cibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
n column: 19
High quality sequence stop: 692.
Location/Qualifiers
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/db_xref="taxon:9606"
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                  BF975096.1 GI:12342311
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                      CACTCTGGACACCACTATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAA-T
                             AAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTTGTAGAAAACC
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KEYWORDS
EST.
SOURCE
Numan.
ORGANISM Homo sapiens
CORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Sizatagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon.9606"
/clone="IMAGE:4846005"
/clone=lib="WIH M44.08"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCAM686 row: b column: 22
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                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.8e-68;
Mismatches 0;
                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.
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In 1 to 670;
In NIH-MGC http://mgc.nci.nih.gov/.
In National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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http://image.llnl.gov
Plate: LLCA1289 row: g column: 13
High quality sequence stop: 650.
Location/Qualifiers
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                                                                                                                                               .234 CAATCATGCGCTGTATGTTTTAATCAGCAGGAAGCATGTTTTTATGTTTGTACAAAGAAG 1293
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                                                                                                                                                                         CCCTTGACGTTTACTTTCAAGTAACACAAACTCTTCCATCAGGCCATGATCTATAGGACC 541
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1694 row: k column: 05
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Pred. No. 1.3e-67;
0; Mismatches 1; Indels 1;
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High quality sequence stop: 693.
Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 99.7%;
Matches 667; Conservative (
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                 /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: Ecorn: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: Ecorn: Cond made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                     Length 670;
                                                                                                                                                                                          4; Indels
                                                                                                                                                                   Score 627.6; DB 12;
Pred. No. 2.3e-64;
0; Mismatches 4;
        /clone_lib="NIH_MGC_48"
/clone="IMAGE:4576548"
                                                                                                                                                                   22.3%;
98.8%;
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l. .956
/organisme"Homo sapiens"
/db_xref="taxon:8606"
/db_xref="taxon:8606"
/clone="InAGE:4309707"
/clone=Lib="NHH_MXC_48"
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/tab_host="DHIB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nlh.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inocyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMIB3 row: i column: 04
High quality sequence stop: 725.
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National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 97.2%; Pred. No. 2.6e-64;
Conservative 0; Mismatches 15;
                                          BF664355.1 GI:11938351
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                                                                                                                 Homo sapiens
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BF664355 956 bp mRNA linear EST 21-DEC-2000 602146013F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309707 5',

DEFINITION

09 1241 GCGCTGTATGTTTTAATCAGCAGAAGCATGTTTTTATGTTTGTACAAAGAAGATGTTA 1300 11		KREWORDS SOURCE Human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 928) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammallan Gene Collection (MGC) JOURNAL Onpublished (1999) COMMENT Email: cgapbs-rémail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: High quality sequence stop: 650.	FEATURES Location/Qualifiers 1. 928 /Organism="Homo sapiens" /db_xref="taxon:9606" /clone="The="ThatBE:456366" /clone="The="ThatBE:456366" /lab_host="Organ: B-cells: Vector: poTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: poTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: PoTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: B-cells: PoTB7; /lab_host="Organ: B-
361 GAGCAGAAGGTAGATCCTAAAAAGCATGGTGACAAATGTTTTATATCAACATC 420 1053 CTTTATTATTTGATTCATT	RESULT 14 AW978582 LOCUS DEFINITION RET390691 MAGE resequences, MAGP Homo sapiens CDNA, mRNA sequence. ACCESSION AW978582 AW978582 AW978582.1 GI:8169850 REYWORDS EST. SOURCE HOME Sapiens CRANYORDS BUKARYOCIS, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 604) AUTHORS Hegde, P., 01, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and	Quackenbush, J. TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray JOURNAL Unpublished (2000) COMMENT Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 394 Seq primer: Corvard. Seq primer: Homo sapiens" J. 604 Actorward. A	Query Match 20.3%; Score 572.6; DB 10; Length 604; Best Local Similarity 97.6%; Pred. No. 6e-58; Matches 581; Conservative 0; Mismatches 14; Indels 0; Gaps 0; Qy 1061 TTTGATTCATTTGAGTTAACAGTGGTGTAAGTGATTGTTTTCTATTCTTTTCCCTGA 1120 Db 595 TTGAATCCATTTGAGTAACAGAACAGTGATTAGTGATTGTTTTTTTT

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982 AGGTAGGATGAGAGGAAGGTAGATCCTAAAAGCATGGTGAGAGGATCAAATG-TTTT 1040
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                                                                                                          GCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGATAGCA
                                          Gaps
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                           Length 928;
                                         Indels
Note: this is a NIH_MGC Library."
163 c 222 g 263 t
                          Score 568; DB 12;
Pred. No. 1.5e-57;
0; Mismatches 5;
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Best Local Similarity 98.6%;
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Sequence 3, Application US/09817180
| Sequence 3, Application US/09817180
| Patent No. 6340584
| Patent No. 6340584
| GENERAL INFORMATION
| APPLICANT: GAN, Weiniu et al. |
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USTILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USTILE OF INVENTION: THEREOF | FILE REPERENCE: CLOOL183 |
| CURRENT APPLICATION NUMBER: US/09/817,180 |
| CURRENT FILING DATE: 2001-03-27 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 280; DB 4;
Pred. No. 3.9e-48;
                       PCT-US95-07201-43
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     TYPE: DNA
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Compugen Ltd.
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Copyright (c) 1993
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ALIGNMENTS

11936 11996 1700 2060 ï 1641 ATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACAC 11651 ACTCCCTTAATGCCAACCTTCCCACCAGGAGAATAAGAATAACCTGGCCAGTTGCTCAC GCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGGAGGATGGCTTGAACACAGGTGTTC 1821 AAGAGAGGGCCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAG - - - - - GACTGGGCACGGTGGCTCACACTGTAATCCCAGCACTTTGGGAGGCCGAG CCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAACCCC GTCTGTACTCAAAATGCCAAAAATTAGCCAGGCGTGGTAGCAGCAGCACCTGTAATCCCAGCT ACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTAAGCT Gaps 14; Mismatches 110; Indels 1941 1701 11771 1881 11877 2001 11,711 8 Q g ò δ ò g δŽ Q δ Ω g

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Sequence Sequence

US-09-729-995-3 US-09-791-211-10 US-09-801-052-3 US-08-520-373D-4 US-08-367-841A-43

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCCGAGCCGGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGG 1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1932 CAAAACCCCGTCTGTACTCAAAATGC-AAAATTAGCCAGGGGGTAGCAGGCACCTGT 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCCCAGCTACTTGGGAGGCTGAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.7%; Score 274.2; DB 4; Length 11811;
Best Local Similarity 79.7%; Pred. No. 5.5e-47;
Matches 350; Conservative 0; Mismatches 83; Indels 6;
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PETENT FILING
SEQ ID NO 7
                                                                                                                                   RESULT 2
US-09-078-294-7/C
Sequence 7, Application US/09078294
Patent No. 6265211
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Sequence 3, Application US/09735934A,

Patent No. 637246B,

GENERAL INFORMATION:
                                                                                                12117 CCAAAAACAAAA 12130
                                                                         2121 AAAAAAAAAGAGA 2134
                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: BAC-F2 contig
US-09-078-294-7
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APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0851
CURRENT APPLICATION UNMBER: US/09/735,934A
CURRENT APPLICATION UNMBER: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                               9.6%; Score 269.8; DB 4;
77.9%; Pred. No. 6.1e-46;
Live 0; Mismatches 92;
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Pred. No. 1e-45;
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Fatent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
ITLE OF INVENTION: ANTISENSE MODULATION OF REC:
FILE REFERENCE: RTS-0207
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
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Matches 339; Conservative
                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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ORGANISM: HOMO
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US-09-798-096-10/C
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13310 ACTGCTTGAAGCCAGAAGTTTGAGACCAGGCTGGGTAACAAACCAAACCAAGACCTATCTGTAC 23251
                                                                                                                                                                                2040 AGGTGGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGC 2099
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                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09978197

Patent No. 6403353

GENERAL INFORMATION:
TYPLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USERENCE: LOGOLIYABIV
TITLE OF INVENTION: THERBOY
CURRENT APPLICATION NUMBER: US/09/978,197

CURRENT PAPLICATION NUMBER: 09/813,817

PRIOR FILING DATE: 2001-10-17
PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                    1860 CCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCC
                                                                          1920 TGGCCAACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGTAG
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                                                                                                                                                                                                                                              22961 GAAACTCTGTCTCAAAAAGAAAAAAAAA 22933
                                                                                                                                                                                                                                 2100 AAGACTCTGTCTCAGAAAAAAAAAA 2128
 23250 TAAAAAATCAGTCAATCA----
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Similarity 78.2%;
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Best Local Similarity 78.2
Matches 351; Conservative
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; ORGANISM: Human
US-09-978-197-3
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LENGTH: 59065
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                                                                                        AGGTTGCAGTGAGCTGAGATCGTGCCATTGCACTCCAGCCTGGGGGACAAAAGTGAGACT 43399
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                                                                                                                                                                                                                                                                                  ACATGGCAAAACCCCGTCTGTACTCAAAATGCAAAATTAGCCAGGCGTGGTAGCAGGCA 1985
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                                      1661 GTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTT
                                                                          -GGGAGGTTGAGGAGGGAGGATGCCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACA
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Mismatches 103;
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Pred. No. 2e-45;
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Best Local Similarity 78.28
Matches 351; Conservative
 Conservative
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; ORGANISM: Human
US-09-813-817-3
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Matches 386;
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1876 CCGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGCCCAACATGCCAAA 1935
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                                                                                                                            1936 ACCCCGTCTGTACTCAAAAATGC--AAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAAT 1993
                                                                                                                                                1994 CCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCA 2053
                                                                                                                                                                                                                                                                 2054 GTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCA 2113
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (3409)
OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
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Patent No. 6387645
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(1820)..(1855)
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(3889)..(3950)
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(6966)..(7138)
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ORGANISM: Homo sapiens
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US-09-350-836B-8/C
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LOCATION:
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                                                                                                                                                                                                                                                 APPLICANT: FORG, Julio
APPLICANT: FORG, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
CURRENT APPLICATION UNMER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PRIOR APPLICATION NUMBER: 09/370,265
PRIOR PRIOR DATE: 1909-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PRIOR DATE: 1999-08-09
PRIOR PRIOR DATE: 1999-08-09
PRIOR PRIOR DATE: 1999-07-09
PRIOR PRIOR DATE: 1999-07-04
PRIOR PRIOR DATE: 1999-07-04
PRIOR PRIOR DATE: 1999-07-04
PRIOR PRIOR DATE: 1999-07-24
PRIOR PRIOR DATE: 1999-07-24
PRIOR PRIOR DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/124,444
PRIOR PRIOR DATE: 1998-07-16
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LOCATION: (3409)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
LOCATION: (9214)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidi
LOCATION: (9303)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidi
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
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LOCATION: (9311)
COTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
US-09-608-285A-8
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                                                                Sequence 8, Application US/09608285A
Patent No. 6335013
                                                                                                                                                                                                                                              Ford, John
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ORGANISM: Homo sapiens
FEATURE:
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GENERAL INCRAMINE:
GENERAL INCRAMINE:
APPLICANT: FORG, John
APPLICANT: FORG, John
APPLICANT: FORG, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: MOTHORS.
FILE REPERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-07-16
EARLIER PLICATION NUMBER: 09/350,836
EARLIER PLICATION NUMBER: 09/350,836
EARLIER PLILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-16
SOFTHARE: PARTICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTHARE: PARTING PATE: 1998-07-16
                                                                                                                                                                                                                         Gaps
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NAME/KEY: misc_feature
COCATION: (9214)

OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
NAME/KEY: misc_feature
COCATION: (9303)

OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
NAME/KEY: misc_feature
COCATION: (9311)

OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
COCATION: (9311)
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Patent No. 6447771
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1442 AAAAATAATAATAAA 7427
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Best Local Similarity 79.0%
Matches 297; Conservative
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1824 -----AGAGAGGCCGGCCTGGTGGTCGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 1875
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LOCATION: (9311)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
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OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
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Best Local Similarity 79.09
Matches 297; Conservative
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FEATURE:
NAME/KEY: CDS
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LOCATION: (2466)..(2555)
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(4896)..(4994)
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LOCATION: (8556)..(8639)
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(6965)..(7138)
CDS
(1280)..(1579)
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1994 CCCAGCTACTTGGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGGTGGAGGTTGCA 2053
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPIDES
FILE REFERENCE: 28110/365A
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR PRILICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1999-07-16
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APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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CDS
(7758)..(7859)
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LOCATION: (2734)..(2877)
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(5326)..(5414)
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CDS
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ORGANISM: Homo sapiens
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LOCATION:
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GTAAGCICAGAICGIGCCGIIGCACICCAGCCIGGGCGACAAGAGCAAGACICIGICICA 2113
                       11102 AAMCGAMCAAAAAGGCYRGGMGTGGTGGCTCAYRCCTRTAATYCYAGCACTTTGGGAGG 11043
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Wenny, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1099-08-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-00-16
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% LOADTION: (13641)
% OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine
US-09-608-285A-42
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9.4%; Score 265.6; DB 4; Length:
Best Local Similarity 79.0%; Pred. No. 3.3e-45;
Matches 297; Conservative 34; Mismatches 34; Indels
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PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-03-19
PRIOR PELLING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR PELLING DATE: 1998-02-04
PRIOR FILING DATE: 1998-07-24
PRIOR PELING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR PELING DATE: 1998-07-16
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; Sequence 42, Application US/09608285A
; Patent No. 6335013
                                                                                      2114 GAAAAAAAAAAAAA 2129
                                                                                                                  PRIOR FILING DATE: 1098-07-10 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 42 LENGTH: 14747
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APPLICANT: Ford, J
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10908 CGAACCTGGGAGGTGGAGGTTGCAGTGAGCCGAGATGGTACCACTGCACTCCAGCCTGGG 10849
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Sequence 1, Application US/08688145
Sequence 1, Application US/08688145
Sequence 1, Application US/08688145
Sequence 1, Application C
SEQUENCE INVENTION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: BAX Promoter Sequence and Screening
Patent No. 5744310
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
                                                                                                                   1970 GCCGTGGTAGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10848 TGACAA-AGTGAAACTCCATCTCAAAGAAAAAAAA 10813
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2090 CGACAAGAGCAAGACTCTGTCTCAGAAAAAAAAAAA 2126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SURTHWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,145
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1951
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell and Flores 4370 La Jolla Village
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3885 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
STREET: 4370 La Joll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Patent No. 645521
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/810,671
CURRENT APPLICATION NUMBER: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2054 GTAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCA 2113
                                                                                                                                                                                                                                                                                                              CCGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1936 ACCCCGTCTGTACTCAAAATGC--AAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAAT 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1994 CCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGGAGGTGGAGGTTGCA 2053
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                                                                                                                                                                                                                                              Query Match
9.4%; Score 265.6; DB 4;
Best Local Similarity 79.0%; Pred. No. 3.4e-45;
Matches 297; Conservative 34; Mismatches 34;
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Pred. No. 1.8e-44;
0; Mismatches 93.
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US-09-608-285A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%;
Best Local Similarity 77.9%;
Matches 356; Conservative (
                                                                                                            LOCATION: (13146)..(13691)
NAME/KEY: CDS
LOCATION: (15702)..(15839)
NAME/KEY: misc_feature
LOCATION: (14871)
                                                             : (11613)..(11728)
: CDS
CDS
(8712)..(8852)
                                              (9831)..(9887)
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US-09-810-671-3
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LOCATION:
NAME/KEY:
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                              NAME/KEY:
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MOLECULE TYPE: DNA (genomic)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1676 GATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGATGCCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCT
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69.1%; Pred. No. 2.3e-43;
tive 0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF REG
FILE REPERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEO ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                    35565 AAAGAAAAAAAAATTAG 35583
                                                                                                                                                                                                                                                                                                                                                    2115 AAAAAAAAAAAAAAAGAG 2133
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Best Local Similarity
Matches 376; Conserv
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US-09-798-096-10
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                                                                                                                                                        GTTGAGGAGGAGGATGGCTTGAACACAGGTGTTCAAGGCCAGCCTGGGCAACATAACAA 1785
                                                                                                                                                                          TCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGA 1905
                                                                                                                                                                                                                                                                                                     GTTTGAGACCAGCCTGGCCAACATGGCAAAAACCCCGTCTGTACTCAAAATGC--AAAAAT 1963
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                                                                                            1666 AAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAG
                                                                                                                   TAGCCAGGCGTGGTAGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGA
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                                                                    Gaps
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CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                Length 3885,
                                                                Indels
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                                Score 259.2; DB 1;
Pred. No. 4.7e-44;
0; Mismatches 129;
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Pred. No. 1.2e-43;
0; Mismatches 89;
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                                9.28;
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                                           Local Similarity 73.4 tes 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 78.8
Matches 346; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 43950
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US-08-688-145-1
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                                Query Match
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Matches
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(without alignments)
10937.110 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              1042519 segs, 733713590 residues
                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seg:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seg:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seg:* Published_Applications_NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Appl Sequence 15, Appl Sequence 15, Appl Sequence 10204, A Sequence 10204, A Sequence 10204, Ap Sequence 10204, Ap Sequence 1020, App Sequence 292, Appl Sequence 292, Appl Sequence 215, Appl Sequence 215, Appl Sequence 215, Appl Sequence 227, Appl Sequence 227, Appl Sequence 227, Appl Sequence 227, Appl Sequence 7, Appli Description US-09-966-880A-70 US-09-966-880A-35 US-09-966-880A-35 US-09-966-880A-15 US-09-966-880A-15 US-09-764-891-5477 US-09-764-891-10204 US-09-764-891-6094 US-09-764-891-6094 US-09-764-891-6094 0 US-09-962-436-292 0 US-09-962-832-119 0 US-09-764-877-2857 US-10-003-295-3 US-10-073-49-1837 US-10-072-349-227 0 US-09-764-855-227 US-09-954-531-180 Length DB 6564 11204 2172 2440 13862 13862 13862 3966 3966 15362 32249 65608 65608 65608 111821 15297 32204 603.4 295.2 295.2 295.2 292.6 284.4 281.4 281.4 281.2 Score Result ě ပပ

Sequence 7, Appli Sequence 2903, Ap Sequence 314, App Sequence 3, Appli Sequence 13, Appli	Sequence 3234, Ap Sequence 3, Appli Sequence 2385, Ap	Sequence 134, App Sequence 306, App Sequence 2225, Ap Sequence 17, Appl	Sequence 1542, Ap Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli	Sequence 8538, Ap Sequence 3, Appli Sequence 79, Appl Sequence 2116, Ap	Sequence 3989, Ap Sequence 5474, Ap Sequence 2698, Ap Sequence 3, Appli Sequence 3463, Ap Sequence 9984, Ap
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: HONGO, TASUNU
APPLICANT: HONGO, TASUNU
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PT 11-371382
PRIOR PELICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-34
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 78
                                    Sequence 7, Application US/09966880A Patent No. US20020164743A1
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NAME/KEY: CDS
LOCATION: (80)...(673)
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LOCATION: (1)...(79)
FEATURE:
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ORGANISM: Homo sapiens
JS-09-966-880A-7
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Length 2818; Indels DB 9; Ouery Match 100.0%; Score 2818; Best Local Similarity 100.0%; Pred. No. 0; Matches 2818; Conservative 0; Mismatches

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APPLICANT: MUTAMATEU, MASAMICHI
APPLICANT: MUTAMATEU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SED ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0 Score 2174.6; Pred. No. 0; 0; Mismatches ; Sequence 35, Application US/09966880A; Patent No. US20020164743A1; GENERAL INFORMATION: . 77.28; Best Local Similarity 99.8 Matches 2177; Conservative ORGANISM: Homo sapiens ; ORGANISM: HOMC US-09-966-880A-35

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	Qy 2537 TTCATAAATTTATAAACTTTAGAAATGATTCTAATAACAACGTATGTAACATTGC 2596	QY 2717 ATAAAATACCAAATAAAATATAAAAGTGATTTATATGAAGTTAAAATAAAAATCAG 2776 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 4 US-09-966-880A-15 ; Sequence 15, Application US/09966880A ; Patent No. US20020164743A1 ; GENERAL INFORMATION: ; APPLICANT: Honjo, Tasuku ; APPLICANT: Muramatsu, Masamichi muri on Informaton, Mayorgi Charles	FILE PEFERENCE: 06501-088001 CURRENT APPLICATION NUMBER: US/09/966,880A CURRENT FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: PCT/JP00/01918 PRIOR FILING DATE: 2000-03-28 PRIOR FILING DATE: 1999-12-27 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR APPLICATION NUMBER: JP 11-371382	FRIOR FILING DATE: 1999-03-29 FRIOR FILING DATE: 1999-03-29 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 TYPE: DNA COGANISM: Homo sapiens US-09-966-880A-15	Ouery Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2172; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 623 CCCCTGTATGAGGTTACGAGACGCATTTCGTACTTTGGACTTTGATAGCAA 682
TCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTAATCAGCAGAAGCATGTTTTTA	30 57 17 50 50	AGGTCAAGGTTTGCTACATTTGTATGTGTGTGTGATGCTTCT TATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAA	1757 GTTCAAGGCCAGCCTGGGCAACATAACAAGATCCTGTCTCTCAAAAAAAA	1877 CGAGCCGGGCGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAA 1936 11111111111111111111111111111111111	TAGGAGAGATCGCTTGAACCCAGGAGGTTT CTCCAGCCTGGCGACAACCCAGGAGGAGA TITITITITITITITITITITITITITITITITITIT	77 AAGGATTGCAAGGAATTGTCCTTATCCAACAAATGTAGGGGGCGATAGGGGGTCCC

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             CTTTGGGACTTTGATAGCAACTTCCAGGAATGTCACACACGATGAAATATCTCTGCTGAA
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US-09-764-891-5477
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                 APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTITON: NOVEL CYTIDINE DEAMINASE
TITLE OF INVENTITON: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: D2001-09-28
PRIOR PELLING DATE: 2000-03-28
PRIOR FILING DATE: 12000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-36
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C or
US-09-966-880A-1
                                                                                                                                                                                                                                                                  US20020164743A1
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)...(2440)
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Similarity
US-09-764-891-10204
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                             Query Match
Best Local Simi
Matches 397;
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       APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 5477
LENGTH: 13862
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF ESC ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEC ID NO 10204
                                                                                                                                                                                                                       Score 295.2; DB 9; Length
Pred. No. 3e-53;
0; Mismatches 133; Indels
                                                                                                                                                                                                                        10.5%;
74.6%;
                                                                                                                                                                                                                        Query Match 10.5
Best Local Similarity 74.6
Matches 397; Conservative
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; ORGANISM: Homo sapiens
US-09-764-891-5477
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TYPE: DNA
ORGANISM: HOMO sapiens
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US-09-764-891-10204
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  Length 13862;
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CURRENT APPLICATION NUCLEIC ACIDS, PROCEINS, and Antibodies
FILE REFERENCE: PAIJOCI
CURRENT APPLICATION NUMBER: US/10/205,428
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/19,65
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-11
                                            Indels
Score 295.2; DB 9;
Pred. No. 3e-53;
0; Mismatches 133;
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FILING DATE: 2000-08-14
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
10.5%;
74.6%;
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15160 AAATTAAAAATATAAAAAAAGCTCTTAGGCCAGGCGTGGTGGCTCACGCCTGTAATCCC 15219
                 1666 AAAACAGAATGATAAAGCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAG 1725
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7364
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Pred. No. 1.1e-50;
0; Mismatches 116;
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TITLE OF INVENTION:
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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Publication No. US20030077808A1
GENERAL INFORMATION:
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Best Local Similarity 75.7%;
Matches 365; Conservative C
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; ORGANISM: Homo sapiens
US-09-764-891-7364
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| Publication No. US20030077808A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: NUMBER: US/09/764.891
| CURRENT PELLING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper | NUMBER OF SEQ ID NOS: 10231
| SOFTWARE: PatentIn Ver. 2.0
| ENGINE OF SEQ ID NOS: 10231
| SOFTWARE: PatentIN Ver. 2.0
| ENGINE OF SEQ ID NOS: 10231
                                                                                                                                Length 13862;
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    or
Remaining Prior Application data removed - See File Wrapper NUMBER OF SEQ ID NOS: 1019
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                                                                                                                             ch 10.5%; Score 295.2; DB 9; 11 Similarity 74.6%; Pred. No. 3e-53; 397; Conservative 0; Mismatches 133;
                         SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1003
LENGTH: 13862
                                                                                 ; ORGANISM: Homo sapiens US-10-205-428-1003
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; ORGANISM: HOMO
US-09-764-891-6094
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US-09-764-891-6094
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Best Local S
Matches 397
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Qy 1860 CCAGCACTTTGGGAGCCGAGCCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCC 1919 bb 43268 CCAGCACTTTGGGAGCTGAGCCGGATCACGAGGTCAGGACTTTGAGCCAGCC 43325 Qy 1920 TGGCCAACATGCGAAAACCCGTTGATCAAAATTAGCCAGGCTGGTAG 1979 111111111111111111111111111111111111	RESULT 12 US-09-962-436-292 i Sequence 292, Application US/09962436 i GENERAL INFORMATION: Cancer Gene Determination and Therapeutic Screening Using Sign; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign; TITLE OF INVENTION: Sets i FILE REFERENCE: 689290-75 i CURRENT APPLICATION NUMBER: US/09/962,436 i CURRENT FILING DATE: 2001-09-25 i PRIOR FILING DATE: 2000-09-25 i NUMBER OF SEQ ID NOS: 568 i SOTANARE: PatentIN Version 3.0 i SEQ ID NO 292 i LENGTH: 65608 i THE SEATURE: i AMBEKEY: misc_feature i OTHER INFORMATION: n=a,t,g or c US-09-962-436-292	Query Match 10.0%; Score 281.4; DB 10; Length 65608; Best Local Similarity 81.2%; Pred. No. 7.8e-50; Atches 376; Gaps 4; Matches 376; Conservative 0; Mismatches 81; Indels 6; Gaps 4; QY 1682 GCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGGAGGTTGAGGAGGAGGAGGAT 1741 D HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1742 GGCTTGAACACAGGTGTTCAAGGCCAACATAACAAGATCCTGTCTCTCAAA 1801 1111	QY 1860 CCAGCACTTTGGGAGGCCGAGCCGGGGGATCACCTGTGGTCAGGAGTTTGAGACCAGCC 1919
	19 TA 15520 31-180 100, Application US 100, Application US 100, Application US 11NVENTION: T: Weaver, Zoe INVENTION: Process INVENTION: Process INVENTION: Process INVENTION: Process INVENTION: 200-77 FILING DATE: 2000-09 FILICATION NUMBER: ULING DATE: 2000-09 PLICATION NUMBER: ULING DATE: 2000-09 PLING DATE: 2000-09	SEQ ID NO 180 LENGTH: 65608 TYPE: DNA ORGANISH: HOMO Sapiens FRATURE: NAME/KEY: misc_feature COCATION: (1)(65608) OTHER INFORMATION: n=a,t,q or c	US-09-954-531-180 Query Match Query Match Best Local Similarity 81.2%; Pred. No. 7.8e-50; Matches 376; Conservative 0; Mismatches 81; Indels 6; Gaps 4; Qy 1682 GCTGCGAACGTGGCAACGCTCATAGTTCTAGCTTGGGAGGTTGAGGAGGAGT 1741	

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1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1815 AAAAGAAAGAGAGGGCGGGGGGGGGGGGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1875 GCCGAGCCGGCCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAA 1934
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US-10-003-295-3

US-10-003-295-3

Sequence 3, Application US/10003295

Patent No. US20020168741A1

GENERAL INFORMATION:

APPLICANT: GAN, Weinlu et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF LOOPING HUMAN KINASE PROTEINS, AND ()

TITLE OF LOOPING HUMAN KINASE PROTEINS, AND ()

CURRENT APPLICATION NUMBER: US/10/003,295

CURRENT FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2055 TAAGCTGAGATCGTGCCGTTGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCAG
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                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                              Length 11821;
                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2857
                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                               ; Sequence 2857, Application US/09764877; Patent No. US20020147140A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            al Similarity 74.4
386; Conservative
                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: HOMO
US-09-764-877-2857
                                 US-09-764-877-2857
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                                                                                                                                                                                                             Sequence 119, Application US/09962832
Patent No. US20020110821A1
GENERAL INFORMATION:
APPLICAMT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturities FILE REFERENCE: 682390-74
CURRENT APPLICATION NUMBER: US/09/962,832
FILE REFERENCE: 68230-74
CURRENT APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1802 AAAAAAAAAAAAAAAAAAGA.--AAGAGAGAGGGCGGGGGGTGGTGGCTCACGCCTGTAATC 1859
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                               1682 GCTGCGAACCGTGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGGAT
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9
                                                                                                                  Indels
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llarity 81.2%; Pred. No. 7.8e-50;
Conservative 0; Mismatches 81; 1
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OTHER INFORMATION: n=a,t,g or
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ORGANISM: Homo sapiens
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Matches 376
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11826 ------GACTGGGCACGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAG 11876
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                                                                                                                                                                                                                                   1821 AAGAGAGGGCGGGGGGGGGGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAG 1880
                                                                                                                  1641 ATTAACTATATAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGCACAC 1700
                                                                                                   Gaps
                                                                                                  14;
                                                                             Length 15297;
                                                                           Query Match 9.9%; Score 280; DB 9; Length 155
Best Local Similarity 74.9%; Pred. No. 6.3e-50;
Matches 370; Conservative 0; Mismatches 110; Indels
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15297
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                                     TYPE: DNA
CORGANISM: Homo sapiens
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Search completed: June 19, 2003, 11:33:58 Job time: 381.09 secs

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-MODEL-frame+_n2p.model -DEV-x1p
-WODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_L/USFPTO_spool_L/USFPG66880/runat_14062003_175523_10297/app_query.fasta_1.9493
-DB-A_Geneseq_101002 -QFMT-fastan -SUFFIX-n2p.raq -MINNATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR SCORE-p-CT -THR_MAX-100 -THR_MIN-0 -ALICGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
-USFR-US09966880_eCGN_1_1_632_erunat_14062003_175523_10297 -NCPU-6 -ICPU-3
-NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAAT -DSPBLOCK-100 -LONGLOG
-DBY TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELCENT-7
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(without alignments)
6475.074 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                  protein search, using frame_plus_n2p model
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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4948
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Perfect score:
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auto immunodeficiency syndrome; IgG subclass selection disorder
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N-PSDB; AAC55312.
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                                 Homo sapiens.
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has cytidine activity similar to APOBEC-1. AID has antiallergic, antianemenic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, Diseage disease, ataxia telangiectasia, common variable immunodeficiency disorder, MIC (major histocompatibility class) class in deficiency disease, AIDS (auto immunodeficiency syndrome), elevated ing disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving constituting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cappended to generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human capped sequence data for this patent did not appear in the printed sequence. The sequence data for this patent did not appear in the printed sequence.
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                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                Novel human diagnostic protein #11923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YT;
                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2001; 2001WO-US08631
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23-AUG-2000; 2000US-0649167
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                               Homo sapiens.
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                                                                          1946 ACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACGGTGATCC 1887
                                                                                                                                                      1767 TGGCCTTGAACACCTGTGTTCAAGCCATCCTCCTCCAACCTCCCAAGCAGCTAGAAC 1708
 2006 CCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGT 1947
                                                                                                                 CTCTCTTTCTTTTTTTTTTTTTTTTTGAGACAGGATCTTGTTATGTTGCCCAGGC 1768
                                                                                                                                                                                           1707 TATGAGGGTGTGCCACGGTTCG------CAGCTTTATCATTCTGTT------ 1668
                                                                                                                                                                                                                                    -------TTGTCACAACTCTCTTATATAGTTAA 1642
                                                                                                                            157 uThralaPheAsnProAsnPheSerThrPheArgLeuLysAsnIleLeuPheMetValAs 177
                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; hinbibi, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atheroscierosis; coronary heart disease; arterial ischaemia;
                          9
                                                  bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinfiammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
              Human secreted protein homologue, SEQ ID NO:1848.
                                                                                                                                                                                                                                                                    1641 TATACCTTTGGGAGAAGCATCACACACATAC 1611
                                                                                                                                                                                                                                                                                       177 nLeu------GluHisAsnTyr 182
                                                                                                                                                                                                                                                                                                                             ABB11478 standard; peptide; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antifungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT;
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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Threation also ratates to vectors and recombinant hest cells comportsing a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of antibodies against the polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby completed and interpretation of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence the invention activities. Including cytokine, cell proliferation or cell differentiation activities; and hence of the invention activities; and hence the invention activities; activito or inhibbin-related activities; chamacochies receptor or ligand activities; chamacochies receptor or ligand activities; chamacochies receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions include with tissue regeneration and customal activities may be used to promote wound the proliferative retinopathy, atheroscierosis, coronary heart disease, creativities may be used in the treatment of viral, immunomodulatory activities may be used in the treatment of viral, immunomodulatory activities may be used in the treatment of viral, conjugate to promote cell growth. Polypeptides with growth factor activity may be used to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2183 AATGCTTCCCCATCCTTCTCT------CCCAAATATTGTTCTCTTTCTCTCT 2136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 -----SerPhePhePheLeuLeuArgTrpSerLeuAlaLeuValAlaGlnAlaGlyGlu 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2135 CTCTCTTTTTTTTTTTTTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTG
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                                                                    Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
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                                                                                                                                                                                                            Claim 20; Page 197; 1963pp; English.
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N-PSDB; ABA08722.
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394.00
71.56%
68.81%
7.98%
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Best Local Similarity:
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            ATTTTGAGTACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCAC 1896
                                                              AGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACGC 1836
                                                                          92
                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimmlant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialamentory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobhuria; burn; wound; brome damage; cartilage damage; antiinflammatory disease; coaqulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                        Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                        Human ORFX ORF3056 polypeptide sequence SEQ ID NO:6112
                                                                                                                | ||| ||| ::: |||||||| aTrpProArgileHisPheLeuTyrTrpLysThrPhePhe 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 5297-5298; 5507pp; English.
                                                                                                                                                                                           AAB43292 standard; Protein; 110 AA
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                           graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2141 CTCTCTCTCTTTTTTTTTTTTTTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCCAGGCT
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therapy;
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75
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31
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Mismatches:
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/label= Leader/Signal peptide
291.384
/label= Mature protein
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Matches:
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334 544 604

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355 GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antinifertility; anticobulant; vasotropic; antidarkinsonian; immunostimulant; dermatological; antinteumatic; antitumor; antillicer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                               545 GAAAGAACTTTCAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
            ATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCAT
                                                                      TGTGAGGACCGCAAGGCTGAGCCCGAGGGCTGCGGCGCTGCACCGCGCGGGGTGCAA
                                                                                                 Secreted human proteins, useful as vaccine for treating various , diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; antiinflammatory; immunosuppressive;
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r RJ, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobs K, McCoy JM, Lavallie E, Collin
Treacy M, Agostino MJ, Steininger RJ,
Clark H, Fechtel K, Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 580-581; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAU39075 standard; Protein; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein lp547_4.
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|LeuArgAlaIleLeu 379
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04-DEC-2000; 2000US-0729674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  supplement, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639363/73.
N-PSDB; AAS59293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The PNs and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, inmulating (e.g. as vaccines) or suppressing activity, hemostatics activity, induminating activity, chemotextic/chemokinetic activity, and thrombolytic activity, chemotextic/chemokinetic activity, and tumor inhibition activity. The PNs are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi. viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting biorhythms or caricadic cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGT 154
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                                                                                                                                                                                                                                                                                                                                                                                                     the amino acid sequence of the lp547_4 protein, which is from the lp547_4 clone isolated from a human adult blood _{\rm CDNA}
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                                                                                                                                                                                       Merberg
                                                                                                                                                                                                                                                                                                            proteins used for
                                                                                                                                                                                 McCoy JM, LaVallie ER, Collins-Racie LA,
Agostino MJ, Steininger RJ;
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Matches:
Conservative:
Mismatches:
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therapeutic, diagnostic and research purposes.
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390.00
61.62%
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                                         99WO-US03458
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99US-0251600
                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                         WPI; 1999-518580/43.
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                                       18-FEB-1999;
                                                                             18-FEB-1998;
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26-AUG-1999
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Treacy M,
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or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in disorders including tissue, skin and organ transplantation and in art-versus-host diseases (GVHD), in the induction of tumnur immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodortal disease, osteoporosis or osteoarthritis, mediated by alzheimer's, Parkinson's diseases, Huntington's disease, amplotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, infammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in premals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
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237 GlnargargGlyPheLeuCysAsnGlnAlaProHisLysHisGlyPheLeuGluGlyArg
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Pred. No.:
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Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autofimune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophila; cardiac infarction; stroke; sepsis; archritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowell disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted proteins and encoding polynucleotides, useful in gene thrapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
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Steininger RJ, Spaulding
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M, Agostino MJ,
Fechtel K;
                          AA.
                                                                                                  Human polypeptide SEQ ID NO 174.
                       ABB55784 standard; Protein; 384
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970S-068379P.
980S-070346P.
980S-070643P.
98US-070755P.
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98US-075038P.
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Clark H, Fe
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STEININGER R
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LAVALLIE E R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLARK H.
                                                                                                                                                                                                                                                                                 US2001039335-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVANS C
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20-DEC-1997;
02-JAN-1998;
07-JAN-1998;
08-JAN-1998;
13-JAN-1998;
22-JAN-1998;
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18-FEB-1998;
30-MAR-2000;
                                                                        14-FEB-2002
                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-1998;
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Wong GG,
                                                 ABB55784;
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(AGOS/)
(STEI/)
(SPAU/)
(WONG/)
(CLAR/)
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(COLL/)
(EVAN/)
(MERB/)
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RESULT 8
             ABB55784
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cycostatic, anti-intiammacory, immunomodulator, vulnerary,
neuroprotective, activin, inhibin, chemotactic, haemostatic, thrombolytic
and anti-inflammatory activity and acting as cytokine modulators,
and anti-inflammatory activity and acting as cytokine modulators,
and anti-inflammatory, tissue growth modulators and/or cadherin
suppressors. The polypeptides and polynuclectides are useful in gene
therapies, particularly for preventing, treating or ameliorating any of
the following diseases: immune deficiency and disorders; e.g. bacterial
or fungal infections, autoimmune disorders, cancer, systemic lupus
crythematosus or graft-versus-host disease; myeloid or lymphoid cell
osteoarthritis; central and peripheral nervous system diseases and
centropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's
disease, amyotrophic lateral sclerosis or Shy-brager syndrome;
candiac infartion or stroke; inflammators, sepsis
or systemic inflammatory response syndrome, ischaemia-reperfusion
crythir, endotoxin lethality, arthritis, inflammatory bowel disease or
crohn's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
               are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynuclectides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AACGGCTGC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCTCTACTTC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 LysPhelleSerLysAsnLysHisValSerLeuCysIlePheThrAlaArgIleTyr--- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTTGTAGAAAACCAT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 | 111::||| | 111::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
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83
31
59
12
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Matches:
Conservative:
Mismatches:
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390.00
61.62%
44.86%
7.88%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                             foliaceus
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                 Human immune/haematopoietic antigen SEQ ID NO:11022.
                                                                                        cytostatic; gene therapy; vaccine; metastasis
               AAM83429 standard; Protein; 119 AA.
                                                                                                                                                                                                                        2000US-0198123
2000US-0205515.
2000US-0209467.
2000US-0215135.
2000US-0216447.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0180628.
2000US-0184664.
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2000US-0218290.
2000US-0220963.
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2000US-0225268.
2000US-0225270.
2000US-0225447.
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2000US-0190076
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                                               07-NOV-2001 (first entry)
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2000US-02257
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                                                                                                                        WO200157182-A2.
                                                                                                         Homo sapiens
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37-JUL-2000;
                                                                                                                                                                                                         16-MAR-2000;
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28-JUN-2000;
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14-AUG-2000;
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14 - AUG - 2000
14 - AUG - 2000
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26-JUL-2000
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22-AUG-20
22-AUG-20
                                AAM83429;
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RESULT 9
       AAM83429
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2000US-0246525.
2000US-0246526.
2000US-0246527.
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2000US-0246532.
2000US-0246609.
                                                           2000US-0233065.
2000US-0234223.
2000US-0234274.
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2000US-0241826.
2000US-0244617.
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2000US-0246475.
2000US-0246475.
2000US-0246476.
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2000US-0236370
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2000US-0237039,
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2000US-0233063
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                       2000US-0232399
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                                   14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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01-DEC-2000;
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08-NOV-2000;
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08-NOV-2000;
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17 - NOV - 2
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amino acid sequences given in AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cuclivity, and can be used in gene therapy and vaccine production. (I) rotations and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting polynucleotides may be used to produce the secreted (I), by inserting the cards into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK87695 and AAM82169 represent invention. AAK84942 to AAK87695 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 11022; 3071pp + Sequence Listing; English.
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78
4
17
10
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                      Ruben SM;
                                                                                     2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.05e-34
388.00
82.00%
78.00%
                    2000US-0251030.
2000US-0251988.
                                                     2000US-0256719
2000US-0251479
                                                                                                                                                                                                2001US-0259678
                                                                                                                                                                                                                                                                      Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                      WPI; 2001-483426/52.
N-PSDB; AAK56210.
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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1832 CCGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCCGGGCGGATC 1891

21 ProGlySerVal-LeuThrProValIleProThrLeuTrpGluAlaGluAlaGlyGlySe

DP OY DP

40

1892 ACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCTGTACTCA 1951

1952 AAATGCAAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATCCCAGCTACTTGGGAGGC 2011

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immune response; reproductive disorder; actinic keratosis;
atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis;
mixed connective tissue disease; myelofibrosis; primary thrombocythemia;
paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
protein; cell proliferation; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression of RNA associated proteins -
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                                                                                                                                                                                                                                 "potential phosphorylation site"
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                                                                                                     Amino acid sequence of a human RNA-associated protein.
                                                                                                                                                                                                                                                                                           "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                          site"
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427
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                                             AAY84437 standard; Protein; 384
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98US-0158720.
98US-0186815.
99US-0128660.
                                                                                     (first entry)
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167
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327
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                                                                                                                          RNA-associated
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N-PSDB; AAA12409.
                                                                                                                                                                                                             Key
Modified-site
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                                                                                    25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman JL,
          100
                                                                 AAY84437;
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                                                                                                                          Human;
                                                                                                                                                                                           Homo
                           RESULT 10
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95 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 IleSerIleLeuThrTyrSerGluPheLysHisCysTrPAspThrPheValAspHisGln 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAGAACTTTCAAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCCCAGACAG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, immuneatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, antherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia
                                                                                                                                                                                                                                                                                                                                                                                                    MetaspProProThrPheThrPheAsnPheAsnAsnGluProTrpValArgGlyArgH1s
                                                                                                                                                                                                                                                                                                                                                                                                                                155 GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TTTGGTTATCTTCGCAATAAG------TTTGGTTATCTTCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 --- AspaspGlnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 TGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCCCGGGGTGCAA
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32
32
32
33
33
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Conservative:
Mismatches:
Indels:
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Page 101-102; 131pp; English.
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                                                                                                                                                                                                                                             2.07e-34
388.00
61.62%
44.32%
7.84%
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                                                                                                                                                                                                     384 AA;
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Best Local Similarity:
                                                                                                                                                                                                                               Alignment Scores:
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 Claim 1;
                                                                                                                                                                                                     Sequence
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of detecting the nucleotides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby yolypeptides of the invention have homology to known proteins, thereby yolypeptides of the invention have homology to known proteins, thereby yolying an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; activity in mmunomodulatory activity; activit or inhibit related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                                 Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
63 uValGluThrGlyPheHisHisValGlyGlnAlaGlyLeuGluLeuLeuThrSerGlyAs 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasctropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein homologue, SEQ ID NO:2463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 306; 1963pp; English.
                                                                                                                                                                                                                                                                                                                   ABB12093 standard; peptide; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                         1829 CTCTCTC 1823
                                                                                                                                                                                                           103 oGluLeu 105
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                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                             ABB12093
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                 The interaction retails to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides we certors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful in advive the supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS9510-AAU33304 represent the amino acid. In treatment of leukaemias. AAUS9510-AAU33304 represent the amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITITITITITITITICIGAGACAGAGICITGCICTIGICGCCCAGGCTGGAGTGCAACGG 2070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuProSerSerTrpAspTyrArgHisProProProTrpProAlaAsn-Phe***PheLe 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                          Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
79
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 524; 765pp; English.
                        human secreted protein #2393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
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386.00
79.61%
76.70%
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                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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Query Match:
                                                                                                                                                                                                                                 WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                  Homo sapiens
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                        Novel
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conditions, receptor or ligand activities; or may be convolved in oncogenesis, cancer cell proliferation or metastasis.

C Depending on their biological activities, polypeptides and nucleotides of conditions, e.g., by protein or gene therapy. Such conditions include disorders, hematopoletic disorders (e.g., myeloid) or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, vascular growth. Polypeptides involved with tissue regeneration and required (e.g., of burns, incisions and ulcers), while those with conditions and ulcers, incisions and ulcers), while those with conditions and ulcers, incisions and ulcers, while those with conditions and ulcers, while those with growth. For example, such polypeptides may be used in the treatment of viral, prowh factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used in the treatment of viral, manipulate stem cells outlure to give rise to neurophithelial cells may be used to augment or replace cells damaged by illness, may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2117 TTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCAGC 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2057 TTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGC 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .997 IGGGATTACAGGIGCCIGCTACCACGCCIGGCTAAI---ITTIGCATTITGAGIACAGAC 1941
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 thrombolytic activities; receptor
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383.50
71.64%
65.67%
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Pred. No.:
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The present sequence is provided in a specification relating to nucleic acid molecules encoding 32 novel human secreted polypeptides. The nucleic acid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and caucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic retinopathy), neurological disorders (e.g. Huntington's chorea, coronary alsorders (e.g. Huntington's chorea, coronary alsorders (e.g. Huntington's chorea, coronary alsorders (e.g. Huntington's chorea, corp. promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may coronary services also be used as DNA probes in diagnostic assays to detect and quantitate coll polypeptides may be used as antigens in the production of antibodies and assays to identify modulators of their expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2093 GTCGCCCAGGCTGGAGGGCACGCACGATCTCAGCTTACTGCAACGTCCACCTCCTGGG 2034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA;
DR;
Human; secreted protein; immunomodulatory; antisclerotic; defamatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antialzhelmers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                            R, Fiscella M, Komatsoulls
Rosen CA, Ruben SA, Soppet
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                                                                                                                                                                                                                                                                                                             Ebner
                                                                                                                                                                                                                                                                                                                      Moore PA, Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                            preventing, diagnosing and/or treat
disease and diabetic retinopathy -
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                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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72.39%
64.93%
7.73%
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Query Match:
                                                                                                              Homo sapiens.
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                                                     1973 CGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTTTTGCCCATGTTGGCCAGGCTGG 1914
                                                                                                          1913 TCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTAC 1854
2033 TTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCA 1974
                                                                     GA;
DR;
                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; immunomodulatory; antisclerotic; dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nostropic; anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
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SA, Soppet
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                                                                                                                                                                               eGlyValSerHisArgAlaArgProGlySerValPheLeu 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Fiscella M,
Rosen CA, Ruben
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Wei P, Florence KA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianterial; antifugal; antihematic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficlency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaquiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in assays to identify modulators of their expression and activity
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Matches:
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381.50
72.39%
64.93%
                                                        310 AA;
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PR 31-WAR-1999; 99US-0127607
PR 31-WAR-1999; 99US-0127607
PR 31-WAR-1999; 99US-0127607
PR 30-ARR-1999; 99US-0127607
PR 30-WAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-60236257

XX

WAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

Theurodegenerative disorders and cardiovascular disease.

CA AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

THE SOLITIC AND ARC77606 encode the proteins given in AAB40237 to AAB43397

CA AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

CA CA AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

CA CA AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

CA CA AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397

CA CA AAC746 to AAC77606 encode the proteins given in AAB40237 to AAB43397

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CA CA AAC746 to AAC77606 encode the proteins given in AAB40237 to AAB43397

CA CA AAC746 to AAC77606 encode the proteins and the AAC77604 to AAC77
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Search completed: June 14, 2003, 18:25:26 Job time : 125.983 secs

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2234 GATCCCTTATTGGCTCCTTACATTTTGTTGGATAAAGCACAATTTCCTTGCAAT----- 2181
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                                                                                                                               16 SeralaThrAlaLeuAlaArgValProLeuHisAlaCysArgGluGlyArgTrpAlaSer 35
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               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity;
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200	1943	104	1883	124	1823	144	
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apolipoprotein B m apolipoprotein B m apolipoprotein B m apolipoprotein B m artifact-warning s alpha-1C-adrenergi serine/threonine-s artifact-warning s gene NF2 protein

gene NF2 protein -B-cell growth fact thromboxane A-2 re probable thromboxa

gene NF2 protein -galactosylceramide

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C; Species: Homo sapless (man)
C; Staverie, J.M.
Personal communication, 1992
A; Reference number: A40201
A; Molecule type: DNA
A; Residues: 1-673 < CLA>
B; Claverie, J.M.
Genomics 12, 888-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potent
A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames in frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion o
                                                                                                                                                                                                                                                                                                                                                                                                                       artifact-warning sequence (translated ALU class F) - human
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Matches:
Conservative:
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S41044
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148249
159577
D40201
S65657
178885
D40201
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A56194
T02670
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A53959
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A60646
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S63464
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-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175525_10329/app_query.fasta_1.9493
-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175525_10329/app_query.fasta_1.9493
-DB=PIR_73 -QFMT=fastan -SUFFIX=h2p.rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=blts -START=1 - FATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MXXLEN-200000000
-USFFUSO9966880_eCGN_1_LA5C_erunat_14062003_1755252_10329 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                            ; Search time 81.1094 Seconds
                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                      protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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Maximum Match 100%
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Fgapop 6.0 , Fgapext
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RESULT 3 A40201 ó g Q q ò δy Dβ ò g á g ò qq g ò g Q δ ò QQ ò ò artifact-warning sequence (translated ALU class C) - human
C;Species: Homo sapiens (man)
C;Species: J.M.
C;Species: J.M.
C;Species: Homo sapiens (man)
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of the C;Comment: Any significant similarity of a predicted protein sequence to a portion of the constants. 2109 2108 CAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCAGCTTACTGCAA 2049 2048 CCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTAC 1989 449 AGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTTTTGCCA 1929 TGTTGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCA 1869 AAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCT--------CTCTCT 1822 509 1821 TTCTTTTTTTTTTTTTTTTTTG------AGAGACAGGATCTTGTTATGTTGC 1774 ******PheValPheGlyGlyPhePhePhePhePheAlaLeuPheLeuPheLeuArg 469 SerArgValAlaGlyIleThrGlyMetGlyArgHisSerTrpLeuIleTyrValPheLeu 409 430 LeuProSerTrpSerProLysValLeuGly***GlnAla***AlaThrThrProSer*** 509 inalaTrpalaAlaileProGly***PheMetTyrPhe*****ArgHisSerPheThrM --TTTCTGAGA -------CCTTGAACACCTGTGTTCAAG CCAGGCTGG------GATAAAGCACAATTT-----GCT 1681 629 Ala 629 450 529 1868 549 2204 2129 1988 1928 1743 RESULT 2 ò a ò g οχ g à g g oy Op ò g à Q οχ g à Q ò g ò g õ

2102 -----CATCCTTCTCTCCCAAATATTGTTCTCTTTCTCTCT 2138 2042 1982 1922 1802 1760 1713 1862 401 421 441 461 481 501 520 artifact-warning sequence (translated ALV class A) - human C;Species: Homo sapiens (man) C;Date: 31-Mar.1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 C;Accession: A40201 382 SerArgThrProGlyLeuMet11eHisProProLeuProProLysValLeuGlyLeuGln LeuIlePheCysIlePheSerArgAsn----GlyValLeuProCysTrpProGlyTrp 2041 CTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCCAAGTAGCTGGGATTACAGGTGCC 1981 TGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTTTTGCCATGTTGGC 539 uThrAlaSerSerThrSerArgValTyrAlaIleLeuLeuProGlnProSerAlaTyrVa 2101 TTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCAGCTTACTGCAACCTCCAC ArgThrMetProSer***PhePheValPheLeuValGluMetGlyPheCysHisValGly 1921 CAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCT 501 rpAspTyrArgArgGluProLeuHisProAla---******PhePhePhePheP 1801 TTTGAGAGACAGGATCTTGTTATGTTGCCCAGGCTGGCCTTG--------402 Ala***AlaThrAlaProArgPhePhePhePhePhePhe********LeuArgGlnSer 1712 AGAACTATGAGCGTGTGCCACGGTTCGCAGCTTTATCATTCTGTTT 1667 lGlyLeuGlnAlaProAlaProCysProAlaAsnPheLeuTyrPhe 2218 CTTACATTTTGTTGGATAAAGCACAATTTCCTTGCAATGCTTCCC 613 100 11 69 39 6 Conservative: Mismatches: Indels: US-09-966-880A-7 (1-2818) x C40201 (1-613) 3.38e-25 348.00 50.92% 45.87% 7.05% personal communication, 1992 Percent Similarity: Best Local Similarity: Query Match: R; Claverie, J.M 520 364 2173 2137 462 1759 559

A; Reference number: A40201 A; Accession: A40201

A.Molecule type: DNA
A.Residues: 1-627 <CLA>
B.Claverie, J.M.
Genomics 12, 838-81, 1992
A.Title: Identifying coding exons by similarity search: Alu-derived and other potentl
A.Reference number: A40200; MUID:92241891; PMID:1572661
A.Contents: annotation
C.Comment: This "warning" entry is a conceptual translation in all 6 reading frames o
in-frame stop codons are shown as 'X'.
C.Comment: Any significant similarity of a predicted protein sequence to a portion of

Alignment Scores:

Alignment Pred. No.	nt Scores:	2.06e-24	Lenath:	627				Alignm Pred. Score:	Alignment Scr Pred. No.: Score:
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S 8								QQ	29
RESULT 4 C40201 artifact C; Specit C; Date: C; Access R; Clave Personal A; Refers A; Acces A; Molecu A; Molecu A; Molecu C; Conten C; Commer C; Commer C; Commer	RESULT 4 C40201 artifact-warning sequence (translated ALU class C) - human C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-20 C;Accession: C40201 R;Claverie, J.M. R;Claverie, J.M. A;Reference number: A40201 A;Residues: 1-613 < CLA> R;Claverie, J.M. Genomics: 12, 838-841, 1992 A;Title: Identifying coding exons by similarity search: Alu-derived and cA;Reference number: A40200; MUID:92241891; PMID:1572661 A;Reference number: A40200; MUID:92241891; PMID:1572661 A;Content: This "warning" entry is a conceptual translation in all 6 reactin-frame stop codons are shown as 'X'. C;Comment: This "warning" entry is a predicted protein sequence to C;Comment: Any significant similarity of a predicted protein sequence to	ce (translated (man) quence_revision 1992 201 992 ding exons by s 200; MUID:92241 g" entry is a c re shown as 'X' ant similarity	ranslated ALU class C) - hur D)	human Lext_c) Sh: Alu S61 Slatior protej	- human #text_change 19-May-2000 rch: Alu-derived and oth 2661 nslation in all 6 readin d protein sequence to a	000 other ling f	: potentiall frames of c	RESULT RASULT ATLIES AND ATLIES AND	RESULT 5 740201 artifact-war. C;Species: H C;Date: 31-M C;Date: 31-M C;Date: 00-M C;Date: 10-M C;Carence A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Reference A;Title: Ide A;Reference A;Conmment: T C;Comment: T In-frame st In-frame st

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, 838-841, 1992
lentifying coding exons by similarity search: Alu-derived and other potent:
number: A40200; MUID:92241891; PMID:1572661
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Any significant similarity of a predicted protein sequence to a portion o
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Homo sapiens (man)
Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
H: F40201
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A; Residues: 1-627 <CLA>R; Claverie, J.M.

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artifactors Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C; Accession: B40201
R; Claverie, J.M.
personal communication, 1992
A; Reference number: A40201
A; Molecule type: DNA
A; Residues: 1-301 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potenti
A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Comment: This "warning" entry is a conceptual translation in all 6 reading frames o in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of C; Comment: Any significant similarity of a predicted protein sequence to a portion of
A; Title: Identifying coding exons by similarity search: Alu-derived and other potential A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Contents: annotation
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C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames of in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of
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Jun 20 09:21:39 2003

Fri

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Educionic artifact-warning sequence (translated ALU class E) - human c) F00201 artifact-warning sequence (translated ALU class E) - human c) Species: Homo saplens (man) c; Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000 c; Accession: E40201 E; A.M.

Piclacerie, J.M.

Personal communication, 1992 A; Reference number: A40201 A; Molecule type: DNA A; Residues: 1-597 CCLA> A; Molecule type: DNA A; Reference number: A40200; MUID:92241891; PMID:1572661 A; Title: Identifying coding exons by similarity search: Alu-derived and other potential A; Reference number: A40200; MUID:92241891; PMID:1572661 A; Comment: This "warning" entry is a conceptual translation in all 6 reading frames of in-frame stop codons are shown as 'X'.

C; Comment: Any significant similarity of a predicted protein sequence to a portion of c; Comment: Any significant similarity of a predicted protein sequence to a portion of
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                                                                                                                                                                                                                   CCCGGCTCG-GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTC 1827
-GlyArgSerThrMetAlaGlnSerHisArgLysLeuCysPheLeuGlySerSerAsnSe 433
                                                                                                                1945 CAGACGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCG
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                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                    ---TAATTTTGCATTTTGAGTACAGACGG
                                                                                                                                                                                                                                                                                                                                            1878 CGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTCTCTT--
                                                                                                                                                                                                                                                        AlaThrMetProCys*********ThrGlnLeuIleLeuPheTyrPhe-TyrArgAlaGl
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R; Claverie, J.M.
                         Alignment Scores:
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GGTGTTCAAGGCCAGCCTGGCCAACATAACA 1785 GInGluAlaLysPheAlaValargleucysHisArgThrProAlaTrp1	RESULT 11 B40201 B40201 artifact-warning sequence (translated ALU c; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 31 war-1992 #sequence_revision 11-C; Accession: B40201 R; Claverie, J.W. Personal communication, 1992 A; Reference number: A40201 A; Molecule type: DNA A; Residues: 1-301 < CLA> R; Claverie, J.W. Genomics 12, 838-81, 1992 A; Title: Identifying coding exons by simil. A; Contents: annotation C; Comment: This "warning" entry is a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a conce in-frame stop codons are shown as 'X'. C; Comment: Similarity: 55.81% Mat. Best Local Similarity: 48.06% Ind. DB: 4.98% Ind. DB: 4.983 TGGCACACGCTCATAGTTCTAGCTGCTTM
alargleucyshishightherialinininining AAAAAAAAAAAAAAAAAAAAAAAAAAA	tifact-warning sequence (translat 50201 tifact-warning sequence (translat 50201 bate: 31-Mar-1992 #sequence_revis 50201 = 1.000201 Accession: B40201 Claverie, J.M. Reference number: A40201 Molecule type: DNA Residues: 1-301 <cla> Claverie, J.M. Residues: 1-301 <cla> Claverie, J.M. Residues: 1-301 <cla> Claverie, J.M. Reference number: A40200; MUID:92 Title: Identifying coding exons b Title: Identifying coding exons b Title: Identifying coding exons b Title: Identifying seding exons b Title: Identifying coding e</cla></cla></cla>
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	artifact wanning sequence (translated And C'Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 11-C;Accession: B40201 R;Claverie, J. M. personal communication, 1992 A;Reference number: A40201 A;Recession: B40201 A;Residues: 1-301 < CLA> R;Claverie, J. M. Genomics 12, 838-841, 1992 A;Title: Identifying coding exons by simil A;Reference number: A40200; MUID:92241891; A;Contents: annotation C;Comment: This "warning" entry is a conce in-frame stop codons are shown as 'X'. C;Comment: Any significant similarity of a conce second similarity: 55.81% Cones Rest Local Similarity: 48.06% Ouery Match: A 1988 US-09-966-880A-7 (1-2818) x B40201 (1-301) Ov 1693 TGGCACACGCTCATAGTTCTAGCTCTT
ACTITIGGAGGCCGAGCCGGCG-GATCACCTGTGGTCAGG 1904	C; Accession: B40201 R; Claverie, J.W. Personal communication, 1992 A; Reference number: A40201 A; Molecule type: DNA A; Residues: 1-301 cCLA> R; Claverie, J.W. Genomics 12, 838 841, 1992 A; Title: Identifying coding exons by simil A; Reference number: A40200; MUID:92241891; A; Contents: annotation multiple a conce C; Comment: This "warning" entry is a conce in-frame stop codons are shown as 'X'. C; Comment: Any significant similarity of a C; Comment: Sories: C; Comment: Similarity: 55.818 Core: C; Comment: Similarity: 48.668 DB: Cs.09-966-880A-7 (1-2818) x B40201 (1-301) Ov 1693 TGGCACACGCTCATAGTTCTAGCTCTT
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CACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAAA 2024	A;Title: Identifying cooling exons by sinit A;Reference number: A40200; MUID:92241891; A;Contents: annotation C;Comment: This "warning" entry is a conce in-frame stop codons are shown as 'X'. C;Comment: Any significant similarity of a Alignment Scores: Pred. No.: C;Comment: Scores: Alignment Scores: C;Comment: Any significant similarity of a Score: Score: Score: C;Comment: Any significant similarity of a Nat. Best Local Similarity: C;Comment: A8.06% C;Comment: A9.06% C;Commen
salacysasnProSerTyrSerGlYGLy***AspArgHTG 265 GGAGGTCGCGTAGCCGCTGCCCTCCGC 2084 ::: ::::	C.Comment: This "warning" entry is a conce in-frame stop codons are shown as 'x'. C.Comment: Any significant similarity of a c.; Comment: Any significant similarity of a c.; Comment Scores: Alignment Scores: Alignment Scores: 2.57e-15 Len Score: 5.01% Con Mat Percent Similarity: 55.81% Con Best Local Similarity: 64.98% Ind DB: 05-09-966-880A-7 (1-2818) x B40201 (1-301) 0v 1693 TGGCAACGCTCATAGTTCTAGCTGCTT
GGAGGTTGCAGTAAGCTGAGATCGTGCCGTTGCACTCCAGC 2084 ::::::::::::::::::::::::::::::::::::	Alignment Scores: Alignment Scores: Red. No.: Score: Score
<pre>gLysGlnSerLeuArg***AspCysAlaIleValLeuArgP 284 CTCTGTCTCAGAAAAAAAAA 2125 : </pre>	ignment Scores: 2.57e-15 ore: 246.50 rcent Similarity: 55.81% ery Match: 4.98% 4.98% 169.966-880A-7 (1-2818) x B40201 (1-3
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nserValSerLysLysLys 297 ision 01-Nov-1996 #text_change 05-Nov-1999 W.: Taub, J.V.; Zellstra-Ryalls, J.H.; Somerville,	rent Similarity: 55.81% st Local Similarity: 48.06% ery Match: 4.98% :
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ision of mov-1990 *Lext_change 05-NOV-1999 W.; Taub, J.V.; Zeilstra-Ryalls, J.H.; Somerville,	1693
W.; Taub, J.V.; Zeilstra-Ryalls, J.H.; Somerville,	
arcinoma 3	Qy 1753 AGGTGTTCAAGGCCAGCCTGGGCAACAT
obs. Manary; translated from GB/EMBL/DDBJ	Db 25 ArgSerSerArgProAlaTrpAlaThr***
NID:9288143; PIDN:CAA39297.1;	QY 1810 AAAAAAAAAAGAGAGGGCGGCGT
	Db 45 Asn***LeuGly******AlaGlyHis
4.35e-16 Length: 254.00 Matches: ty: 70.79% Conservative: arity: 61.80% Mismatches: Indels:	GAT
Gaps: * 138022 (1-196)	
AGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCTGTACTC 19	Qy 1972 CGTGGTAGCAGGCACCTGTAATCCCAGCTA
22	104 yMetValAlaAsnIleCysAsnPros
AAAATGCAAAAATTAGCCAGGCGTGGTAGGAGGCACCTGTAATCCCAGCTACTTGGGAGG 2010	2032
	UD 124 *AspeinGlurneLysinfserLeu 13
CTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTAGCAGTAAGCTGAGATCGTGC 2070 	lin I - human (fragment)
GTTGCACTCCAGCCTGGGCGACAAAGAGCACTCTGTCTCAGAAAAAAAA	C;Date: ZI-Dec-1996 #sequence_revision 06-Ju C;Accession: G01233
	R; Madsen, P.P. submitted to the EMBL Data Library, Decemb
GAGAGAGAGAGAAAGAAAGAAAT 2155	A;Reference number: G06330 A;Accession: G01233
Cancer Res. 50, Afritle: A human A; Accession: 138 A; Accession: 138 A; Catatus: prelim A; Molecule type: 1-19 A; Cross-referenc Alignment Scores Percent Similari Best Local Similari Best Local Similari Cuery Match: DB: Cy 1891 CA Oy 1891 CA Oy 2011 CT	9, K.; Vieira, W.; Taub, J.V.; Zeilstra-Ryalls, J.H.; Somerville, 58-5667, 1990 254-5667, 1990 3.0-kilobase DNA sequence transforms both i 138021 2.

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ry is a conceptual translation in all 6 reading frames own as 'X'. Milarity of a predicted protein sequence to a portion of
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UID:92241891; PMID:1572661
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                       _revision 11-Aug-1995 #text_change 19-May-2000
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA a:Daciding: 1-116 June	20 pCysAspLeuGlySerLeuLysSerProProPro-GlySerSerAspSerProAlaSerA
A; residues: 1-110 <mad> A; Cross-references: EMBL:U03891; NID:9436940; PIDN:AAA03706.1; PID:9436941 C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1</mad>	QY 2010 CCTCCCAAGTAGCTGGGATTACAGGTGCCTACCAACGTGGTAATTTTTGCATTTT 1951
Alignment Scores: Pred. No.: 2.98e-15 Length: 116 Score: 245.00 Matches: 51 Percent Similarity: 61.82% Conservative: 17 Best Local Similarity: 46.36% Mismatches: 10 DB: 2 Gaps: 3	Oy 1950 GAGTACAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCCTCAACCAGGTG 1891
US-09-966-880A-7 (1-2818) x G01233 (1-116)	Qy 1830 CCTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Qy 305 TACCGCGTCACCTGGTTCACCTCGGAGCCCCTGCTACACTGTGCCCGACAT 358	Db 90 rgAspLeuPhePhePhePhePhePhePhePhePhePhePhePhePheP
Oy 359 GTGGCCGACTTTCTGCGAGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCCTC 418	A53853 Apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4) - rabbit c; Species: Oryctolagus cuniculus (domestic rabbit) C; Species: O7-Oct.1994 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000
Oy 419 TACTICTGTGAGGACGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCAC 469 1	C;Accession: Asiabis C;Yaconaka, S.; Poksay, K.S.; Balestra, M.E.; Zeng, G.Q.; Innerarity, T.L. J. Balol. Chem. 269, 21725-21734, 1994 A;Title: Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc mott
Oy 470 CGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACT 529	ributed. A.Reference number: A53853; MUID:94342367; PMID:8063816 A.Accession: A53853 A.Status: preliminary
Qy 530 TITGTAGAAAACCAIGAAAGAACTITCAAAGCCIGGGAGGGCTGCAFGAAAATTCAGTT 589	A:Molecule type: mRNA A.Residues: 1-236 <2AM- A)Cross-references: GB:U10695; NID:9506180; PIDN:AAA56718.1; PID:9506181 C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
Qy 590 CGTCTCCAGACAGCTTCGGCGCATCCTT 619	C; Keywords: hydrolase; zinc Alignment Scores: 3.12e-13 Length: 236
RESULT 13 A46010 X-linked retinopathy protein (C-terminal, clone XEH.8c) - human (fragment) C:Species: Homo sapiens (man)	Score: 225.00 Matches: 49 Percent Similarity: 57.25% Conservative: 26 Best Local Similarity: 37.40% Mismatches: 48 Query Match: 4.55% Indels: 8 DB: 2
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Accession: A46010 R;Wong, P.; MacDonald, I.M.; Sood, R.; Smith, C.; Pilon, R.; Tenniswood, M.	US-09-966-880A-7 (1-2818) x A53853 (1-236)
Genomics 15, 467-471, 1993 A;Title: Identification and partial characterization of a candidate gene for X-linked reA;Reference number: A46010; MUID:93224131; PMID:8468040 A;Arcession: A46010	Oy 149 CGGCGTGAGACCTGTGCTAGTGAGGGGGGGGGGGGGGGTACATCCTTTCA 208 :::
A; Notecule type: nucleic acid A; Residues: 1-100 <won></won>	Qy 209 CTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTC 265
A;Cross-references: GB:S58722; NID:g299470; PIDN:AAB26149.1; PID:g299471 A;Note: sequence extracted from NCBI backbone (NCBIN:129339, NCBIP:129340)	266CGCTACATCTCGGACTGGGACCTGGCCGCTGCTACCGCGTCACCTGGTTC
Pred. No.: 4.55e-15 Length: 100 Score: 243.00 Matches: 63 Percent Similarity: 65.18% Conservative: 10 Best Local Similarity: 56.25% Mismatches: 27 Ouerv Match: 4 42%	OB GIULYSLEUTHINESIGIUGIYATYLEUGIYFIOSETINICYSCYSSELITETHITIPFHE 07 QY 323 ACCTCCTGGAGCCCTGCTACGACTGTGCCGGACTTTCTGCGAGGAAC 382
2.25. thorse. 0A-7 (1-2818) x A46010 (1-100)	Qy 383 CCCAACCTCAGTCTGAGGATCTTCACCGCGCCCTCTACTGTGAGGACGCAAGGCT 442
Qy 2130 TITITITITITITICIGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACG 2071	Qy 443 GAGCCCGAGGGCTGCGCGCGCGCGGGGGGGGAATAGCCATCATGACTTC 502
Oy 2070 GCACGATCTCAGCTTACTGCAACCTCCACCTCGGGTTCAAGCAATTCTCCTGCCTCAG 2011	Qy 503 AAAGATTATTTACTGCTGGAATACTTTTGTA 535 :::

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C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: 54104
R:Yeo, J.P.: Alderuccio, F.; Toh, B.H.
Nature 367, 288-291, 1994
A:Title: A new circonosomal protein essential for mitotic spindle assembly.
A:Reference number: 541044; MUID:94166884; PMID:8121495
A:Reference number: 541044
A:Residues: Preliminary
A:Molecule type: mRNA
A:Residues: 1-418 < YEO>
C:Superfamily: human 48.2K chromosomal protein
C:Reywords: chromosomal protein
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64
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Matches:
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147 SerGluTyrCysTyrCysTrpGluAsnPheVal 157
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Search completed: June 14, 2003, 18:56:28 Job time: 98.1094 secs

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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claverie J.-M.; "Identifying cooling exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quentin Y.;
"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                                                                                                                                                        Q05481 h
094966 h
Q02732 s
P30020 b
                             P49646
P41238
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P51957
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P37198
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Q9nq38
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P09144
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042280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 31, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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TA2R_HUMAN
PKP2_HUMAN
                                                          ABME_MOUSE
ABME_RAT
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Z195_HUMAN
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ABME_HUMAN
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WN14_CHICK
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PSAB_CHLRE
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UBPJ_HUMAN
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ATIN_HSVBP
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IF4G_RABIT
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SEQUENCE FROM N.A.
MEDLINE-95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed-3138422;
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CONCEPT
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-MODEL=frame+_n2p.model -DEV-x1p
-MODEL=frame+_n2p.model -DEV-x1p
-Q=/Cqn2_1/USPTO_spool/USC9966880/runat_14062003_175524_10304/app_query.fasta_1.9493
-Q=/Cqn2_1/USPTO_spool/USC9966880/runat_14062003_175524_10304/app_query.fasta_1.9493
-DB=Swissprot_40 -QFWT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MARTEX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UNEN=USC966880_eCG_1_1_196_erunat_14062003_175524_10304 -NCPU=6 -ICPU=3
-USER=USC9966880_eCG_1_1_196_erunat_14062003_175524_10304 -NCPU=6 -ICPU=3
-USER=USC9966880_eCG_1_1_196_erunat_14062003_175524_10304 -NCPU=6 -ICPU=3
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-USER=USC996880_eCG_1_1 - 196_erunat_14062003_175524_10304 -NCPU=6 -ICPU=3
-USER=USC996880_eCG_1_1 - 196_erunat_14062003_175524_10304 -NCPU=6 -ICPU=3
-USEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2003 Compugen Ltd
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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESOLTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH CORRESCUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed 'Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                           MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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                                391 ProproArgProAla*******PhePhe***AspGlyValSerLeuLeuProArg 410
                                                                                                411 LeuGluCysSerGlyAlaIleSerAlaHisCysAsnLeuArgLeuProGlySerSerAsp 430
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                                                                                                                                                                431 SerProAlaSerAlaSerArgValAlaGlyIleThrGlyAlaArgHisHisAlaArgLeu
                                                                                                                                                                                                                     "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SP sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
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1844 CCACCACGCCCGGCCCTCTCTTTTTT-
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MEDLINE=95021758; PubMed=7935834;
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MEDLINE-88333009; PubMed-3138422;
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MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljevic A.;
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"Alu alert.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                  1814 TITITITITITITITGAGAGACAGGATCTTGTTATGTTGCCCAGGCTGGCCTTGAACAC
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(Rel. 40, Last annotation update)
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
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MEDLINE-88333009; PubMed-3138422;
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
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PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED RESIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREEMPRYS (ESPECTALLY SITUATED ON THE CONFLEMENTARY STRAND) HAVE A CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPREPATION OF SEQUENCE OF AN THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH
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"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HATE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
Alu subfamily SQ sequence contamination warning entry.
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165 AsnArgLeuAsnProGlyGlyGlyGlyCysSerGluProArgSerArgHisCysThrPro 184

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BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
          OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MY COMPAIN ALCI-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESCULED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POLINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSEQUENCE OF ERRONEGUS ALU-DERIVED AMINO ACID SEQUENCES
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J. Mol. Evol. 32:105-121(1991).

-i. MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
-i. MISCELLANEOUS: PALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                593 AA
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Genomics 12:838-841(1992).
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MEDLINE-91178815; Pubmed-1706781;
Jurka J., Milosavljevic A.;
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MEDLINE-88333009; PubMed-3138422;
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FRAME-2.
FRAME-3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Alu subfamilly J sequence contamination warning entry.
Homo sapiens (Human).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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J. Mol. Evol. 27:194-202(1988).
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"Identifying coding exons by similarity sear potentially misleading protein sequences.";
Genomics 12:838-841(1992).
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
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ACID SEQUENCES.

-- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5° OR 3' UNTRANSLATED REGIONS. HOWEVER, LIGATED MITH ALU-DERIVED SEQUENCE IN ANY OR REATRANGED CONAS LIGATED MITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
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MEDLIES LASSIFICATION.

JULKA J., MILLOSAVIJEVIC A.;

"Reconstruction and analysis of human Alu genes.";

"Reconstruction and analysis of human Alu genes.";

J. MOI. Evol. 32:105-121(1991).

"MISCELLANDEOUS: WARRIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
CONSENSUS SEQUENCES FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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            1693
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01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Alu subfamily J sequence contamination warning entry.
1732 CCTCAACCTCCCAAGCAGCTAGAACTATGAGCGTGTGCCA
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MEDLINE-88333009; PubMed-3138422;
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Nature 371:752-752(1994).
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P39188:
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CODING NUCLEOTIDE SEQUENCE.

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                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ACID SEQUENCES.

CAUTION: ALLO REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERTAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSCRIPTS MAY CONTAIN LIBRATIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CUDAS.

LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL. TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

OCNSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
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MEDLINE-91178815; Pubmed=1706781;
Jurka J., Milosavljevic A.;
Jurka J., Milosavljevic A.;
J. Mol. Evol. 32:105-121(1991).
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL ITYO 8 SUBFAMILIES. THEREFORE,
CONSENSIS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
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MEDLINE-88333009; PubMed-3138422;
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MEDLINE-95021758; PubMed-79358
Claverie J.-M., Makalowski W.;
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Nature 371:752-752(1994).
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or send an email to license@isb-sib.ch).
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CAUTION: ALL REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CUNA LIBRARIES ALSO CONTAIN PRETIAL AND/OR REARRANGED CONAS.

LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION ALTHOUGH ALU LIGATED WITH ALU-DERIVED SEQUENCE IN THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
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THAT ALU REPEATS FALL INTO 8 SUBFANLIES: THEREFORE, 8 ALU WARNING
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FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-91178815; PubMed-1706781;
Jurka J., Milosavljavic A.,
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
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15-JUN-2002 (Rel. 41, Last annotation update)
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MEDLINE-88333009; Pubmed-3138422;
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"Alu alert.";
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                                                                                                                                                                                                                                                                                                                                        STANDARD;
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P39195;
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CONCEPT.
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NCBI_TaxID=9606
                                                                                                                                                      Claverie J.-M.;
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                                                                                                                                  CONCEPT
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                           CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
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         CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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Hypothetical protein.
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J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANBOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           Alu subfamily SC sequence contamination warning entry.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Jurka J., Milosavljevic A.;
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MEDLINE-95021758; PubMed=79358:
Claverie J.-M., Makalowski W.;
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ALU FAMILIES CLASSIFICATION
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-1. CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPES MAY CONTAIN ALLU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOMEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN RADING FRAME MAY HAVE RESOLTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING THE CONSEQUENCE OF SHOULD OF SEQUENCING THE CONSEQUENCE OF SERVENCING THE CONSEQUENCE OF SERVENCING THE CONSEQUENCE OF BRRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHE POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        waves of fixation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALU FAMILIES CLASSIFICATION.
MEDLINE-91178815; PubMed-1706781;
MIDSavljevic A., Milosavljevic A.,
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Alu family developed through successive waves closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
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                                                     MEDLINE=95021758; PubMed=7935834;
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                                                                                                                                                                                                                                                           MEDLINE=92241891; PubMed=1572661
                                                                                             Claverie J.-M., Makalowski W.;
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SEQUENCE FROM N.A.
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                                                                                                                            'Alu alert.
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uLeuThrSer**--SerAlaArgLeuGlyLeuProLysCysTrpAspTyrArgArgGlu 386
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                                                                                                                                          CCTGTGTTCAAGCCATCCTCCTCCTCAACCTCCCAAGCAGCTAGAACTATGAGCGTGTG
                                                                                          TCTCTCTCTCTCTTTTTTTTTTTTTTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alu subfamily SC sequence contamination warning entry.
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Matches:
Conservative:
Mismatches:
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-95021758; PubMed-7935834;
Claverie J.-M., Makalowski W.;
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ALU FAMILIES CLASSIFICATION.
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Nature 371:752-752(1994).
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Best Local Similarity:
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Alignment Scores:
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ACID SEQUENCES.

-1- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CONA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REBRRANGED CDNAS. LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSTBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING RAPIFEACT OR MAY BE DUE TO MISSINTERREPATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOCKED ON SEVERAL OCCASIONS, WITH CONSEQUENCE OF ERRONBOUS ALU-DERIVED AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALD-TRANSLAFED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE HATA ALU REPEATS FALL INTO 8 SUBFAMILIES. THERREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT COWTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANGOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP COODN, 'XXX' IS USED TO SEPRATE THE VARIOUS TRANSLATION PHASES. CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
"The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
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46EE8C4F493650A7 CRC64;
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"Ducka J., Milosavljevic A.,
"Reconstruction and analysis of human Alu genes.";
J. MOL. Evol. 32:105-121(1991).
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FRAME-2.
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A MEDINE-2005/165; Pubmed-10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Bebages A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Almeida J.P., Bebbage A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Barrill W.D., Burtron J., Carder C., Carter N.P., Chen Y., Clark

RA Burrill W.D., Burron J., Carder C., Carter N.P., Chen Y., Clark

RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Conroy D., Corby N.R., Fleming K., French L., Garner A.A., Holmer A.G.,

RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martyn I.D., Mashreghl: Mohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashreghl: Mohammadi M., Matthews L.H., Mcrann O.T.,

RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Williams L., Williams C., Williams C., Williams S.A., Wasakak R., Asakawa S., Kodoh J., Loo, Charley S., Rogers J., Shintan I., Lao H.I.,

RA Parish C.L., Hubbard T., Bentley D.R., Askawa S., Roder S., Roder S., Do A., Do T.,

RA Parish C.L., Flaug F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
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Catarrhini; Hominidae; Homo.
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RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Pan Ban S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Ray Mang Q., Wang Y., Wang Y., Wang Y., Mang Y., Mang Y., Mang Y., Mang Y., Mang Y., Mang Y., Malax D., Waray J., Milar N., Minx P., Pulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goelab D., Graves T., Hawkins J., Rah Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Rochet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Wilson R., Ram K., Tahai J., Mardis E., Waterston R., Wilson R., Ram Carden M., Roder M., Kedra D., Ram Carden M., Redra D., Ram Carden M., Redra D., Ram Carden M., Simon M.I., Dumanski J.P., Peyrard M., Redra D., Ram Linison P., Bodentelch A., Hartman K., Hu X., Khan A.S., Lane L., The DNA sequence of human chromosome 22.";

Nature 402:489-495(1999).
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"Molecular cloning of phorbolin 3.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYIDYLATE DEAMINASES
-!- SIMILARITY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-! OR MET-148 IS THE
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InterPro; IPR002125; dCMP/cyt_deam
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102 IGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGA 355
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                                                                                                                  LeuMetAspProHisIlePheThrSerAsnPheAsnAsn-----GlyIleGlyArg
                                                                                                                                                CGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTG
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"Identifying coding exons by similarity search: alu-derived and other
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
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Genomics 12:838-841(1992).
                                                           US-09-966-880A-7 (1-2818) x PHB1_HUMAN (1-199)
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MEDLINE=95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
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ALU FAMILIES CLASSIFICATION
 43.468
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                                                                                  312 IleTyr------AspTyrAspProLeuTyrLysGluAlaLeuGlnMetLeu 326
                                                                                                                                  ACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCA 586
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                  467 CACCGCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAAT
                                                        CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGCGGCTG
356 CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H., Dumanski J.P., Tommerup N., Collins J.E., Wright C.L., Dunham Macginnitle A.J., Davidson N.O., Celis J.E.; Psoriasis up-regulated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1."; J. Invest. Dermatol. 113:162-169(1999).
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                                                                                                                                                                                                                                                   367 GlnAlaLeuSerGlyArgLeuArgAlaIleLeu 377
                                                                                                                                                                                                                                                                                                                        PHB1_HUMAN STANDARD; PRT; 199 AA. P31941; 012807; 01-JUL-1993 (Rel. 26, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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Aarhus/Ghent-2DPAGE; 2116; IEF.
InterPro; IPR002125; GCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 53-60; 112-121 AND 129-137.
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MEDLINE-99399284; PubMed-10469298;
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MEDLINE=93162043; PubMed=1286667;
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58,12%
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                             PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIEDED BY POLITI. NORMAL TRANSCRIEDED BY THEM ARE ACTIVELY TRANSCRIEDED BY POLITI. NORMAL TRANSCRIEDEN MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.

CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPREPATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOKED ON SEVERAL OCCASIONS, WITH
                                                                                                                                                                                     J. MOI. EVOI. 32:105-121(1991).
-I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBRAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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                                                                                                                                                                                                                                                                                                                          TRANSLATION PHASES.
TO AVOID THE FURTHER
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                                     The Alu family developed through successive waves of fixation
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46
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                                                                                                            ALU FAMILIES CLASSIFICATION.
MEDLINE-91178815; PubMed-1706781;
MILOSAVIJEVIC A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
                                                                                                                                                                                                                                                                                                                        CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER
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Matches:
Conservative:
Mismatches:
                                                         connected with primate lineage history. Evol. 27:194-202(1988).
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FRAME-2.
FRAME-3.
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MEDLINE-88333009; PubMed-3138422;
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-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                            327 sSerProAlaSerAlaSerGlnValAlaGlyThrThrGlyAlaArgHisTyrAlaArgLe
                                                                                                   1964 AATTTTGCATTTTGAGTACAGACGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACT
                                                                                                                    1904 CCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAG
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                                          2024 TTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-88333009; Pubmed=3138422;
Quentin Y.;
"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
Homo sapiens (Human).
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
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MEDLINE-95021758; Pubmed-7935834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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P39190;
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-!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODOM, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
-!- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
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- ACID SEQUENCES.

 --- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND PRIMATE CENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER, COBMA LITERARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDRAS LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A CREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS, CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE OF AN ALU IN AN OPEN REDDITE FRAME MAY HAVE RESULTED FROM A CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH THE CONSIDERATION.
 - BEING REPORTED.
 CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE CODING NUCLEOTIDE SEQUENCE.

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85C4155726DEF235 CRC64; FRAME-1. FRAME-2. FRAME-3. FRAME-4. FRAME-6 EMBL; U14569; .; NOT_ANNOTATED_CDS. Hypothetical protein.

DOMAIN 1 96 FPANET 63573 MW; 194 292 391 489 587 AA; SEQUENCE DOMAIN DOMAIN NIWWO DOMAIN

587 84 14 42 10 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.29e-24 358.00 65.33% 56.00% . 248 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

US-09-966-880A-7 (1-2818) x ALU3_HUMAN (1-587)

οy	1693	1693 TGGCACACGCTCATAGTTCTAGCTGCTTGGGAGGTGAGGAGGAGGATGCCTTGAACAC 1752	1752
Db	148		167
Οÿ	1753	3GCCAG	1797
Dp	167		186
Qy	1798	GAGC	1857
qq	186	186 pargalaargLeuArgLeuLygLyg********ProGlyAlaValAlaHisAlaCysAs 206	206
Qy	1858	1858 TCCCAGCACTTTGGGAGGCCGAGCCGGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAG 1917	1917
Dp	206		225
٥y	1918	1918 CCTGGCCAACATGGCAAAACCCGTCTGTACTCAAAATGCAAAAATTAGCCAGGCGTGGT 1977	1977
Db	226	226 ProGly***AsnGlyGluThrProSerLeuLeuLysIleGlnLysLeuAlaGlyArgSer 245	245

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2097
1978 AGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCA 2037
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                 246 GlyGlyArgLeu***SerGlnLeuLeuGlyArgLeuArgGlnGluAsnGlyValAsnPro 265
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Search completed: June 14, 2003, 18:29:28 Job time : 55.3473 secs

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99had8 homo sapten

98wtz3 homo sapten

97825 homo sapten

99hbs7 homo sapten

99y47 homo sapten

99y47 homo sapten

99y45 homo sapten

99p195 homo sapten

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Q9h5r3 homo s
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-20460541; PubMed=11007475;
Revy P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O.,
Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,
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Q96eb1 P
Q9ha67 P
Q9y235 P
Q9bvd9 P
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Q9h6g8 1
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Last annotation update)
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MEDLINE=20408890; Pubmed=10950930;
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(TrEMBLrel. 16, I
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 Homo sapiens (Human).
NCBI_TaxID=9606
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01-MAR-2001 (
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-Q-CQ012_1/10216/app_query.fasta_1.9493
-Q-CQ012_1/102PO_spool/UG09966880/runat_14062003_175524_10316/app_query.fasta_1.9493
-Q-CQ012_1/102PO_spool/UG09966880/runat_14062003_175524_10316
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THE_SCOREP-DCt -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-UOSER-GOOLIGN-200 -THE PEOPESTER-500 -MINIEN-0 -MAXIEN-20000000
-USER-US09966880_CGCN_11_978_erunat_14062003_175524_10316 -NCPU-6 -ICPU-3
-NO_MAPP -LARREQUERY NEG_SCORES-0 -WAIT -DSPEDCOK-100 -LONGLOG
-PBV_TRECUT-120 -WARN_TIMEOUT-30 -THRADD-1 -XGAPEXT-0 - XGAPEXT-7 - YGAPOP-10 -YGAPEXT-0.5 -DELCOP-6 -DELEXT-7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Fgapop 6.0 , Fgapext
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Tezcan I., Ersoy F., Kayserili H., Ugazio A.G., Brousse N.,
Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer
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                        cytidine deaminase (AID) deficiency causes form of the Hyper-IgM syndrome (HIGM2).";
                                                                          Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB040431; BAB12721.1;
EMBL; AB040430; BAB12720.1;
EMBL; BC006296; AAH06296.1;
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1
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                        "Activation-induced autosomal recessive
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Best Local Similarity:
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                                                                                                                                              SEQUENCE FROM N.A. MEDIATE STATES; MEDIATE S., Sugai M., Kinoshita K., Manamatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K., Davidson N.O., Honjo T.; Sugai M., Kinoshita K., Specific expression of activation-induced cytidine deaminase (AID), novel member of the RNA-editing deaminase family in germinal center cells.
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
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EMBL; AF132979; AAD41793.1; -
MGD: MGI:1342279; A1cda.

Interpro; IPRO02125; GCMP/Cyt_deam.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           198
183
6
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0
01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Activation-induced cytidine deaminase.
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Matches:
Conservative:
Mismatches:
Indels:
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1008.00
95.94%
92.89%
20.37%
                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                  AICDA OR AID.
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GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TTTGGTTATCTTCGCAATAAG-------AACGGCTGC 244
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                                                                                 Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z.; "Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF182420; AAG14956.1; -.
EMBL; BC024268; AAH24268.1; -.
                                                                                                                                                                                                                                               CRC64;
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83
31
59
12
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1
SEQUENCE 384 AA; 46408 MW; 60525DC3B7D903D6
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Conservative:
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Indels:
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                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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|LeuArgAlaIleLeu 379
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390.00
61.62%
44.86%
7.88%
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              Homo sapiens (Human)
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
                                                                                                                                                 SEQUENCE FROM N.A.
                                               NCBI_TaxID=9606;
                                                                                                                                                           TISSUE-SKIN;
Strausberg R.;
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EMBL; AKO25116; BAB15071.1; -- SEQUENCE 171 AA: 18436 MW; DDC546D275038FAF CRC64;
                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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90
16
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17
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MDS019 (Phorbolin-like protein MDS019).
                                                      ol-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) CDNA: FL021463 fis, clone COL04765.
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Matches:
Conservative:
Mismatches:
Indels:
                        171 AA
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                        PRT;
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                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                             2.7e-33
403.50
74.13%
62.94%
8.17%
                        PRELIMINARY;
                                                                                                Homo sapiens (Human)
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Best Local Similarity:
Query Match:
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                       LISSUE-COLON;
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ID Q9H728
AC Q9H728;
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RESULT 3
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Percent Similarity:
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                                                                                                          Alignment Scores:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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OJONZI7;
OJONZI7;
OJOCT-2000 (TEMBLrel. 15, Last sequence update)
O1-0CT-2000 (TEMBLrel. 15, Last sequence update)
O1-0CT-2000 (TEMBLrel. 15, Last annotation update)
O1-0CT-20489 fis, clone KAT08285 annotation update)
HOMO Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(1)
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136 AA; 14980 MW; D2336B649A110163 CRC64;
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73
8
19
1
                    096NR6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ30278 fis, clone BRACE2002755.
Homo sapiens (Human).
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Matches:
Conservative:
Mismatches:
Indels:
                 136 AA.
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389.00
80.20$
72.28$
7.86$
              PRELIMINARY:
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SEQUENCE FROM N.A.
TISSUE=CEREBELLUM;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A.

Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00496; BAA91205.1;
SEQUENCE 239 AA; 25728 MW; 5272FFA2C34214A5 CRC64;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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Qy 224 CTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCGCTAC 271	OY 272 ATCTGGGACTGGGACCTAGACCCTGCCTGCTACCGCGTCACCTGGTTCACCTCTGG 331	Db 89 PheCysAspAspIleLeuSerProAsnThrLysTyrGlnValThrTrpTyrThrSerTrp 108 Qy 332 AGCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGAACCCCAACCTC 391	Db 109 SerProCysProAspCysAlaGlyGluValAlaGluPheLeuAlaArgHisSerAsnVal 128	Ay 392 AGTCTGAGGATCTTCACCGGGGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG 451 ::: ::	452 GGGCTGCGGCGGCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT	Db 148 GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 167 Qy 512 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG 571	Db 168 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProfrpLysGly 187 Qy 572 CTGCATGAAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATCCTT 619		RESULT 9	ID ODEGW3 PRELIMINARY; PRT; 122 AA.			RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., RA Subaki Y., Sugano S., Hashimoto K.; Dr. "Inclation of full locate cross from mecanic brain only	libraries.": Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB0555293; BAB21918.1;	KW Hypotherical protein. SQ SEQUENCE 122 AA; 13539 MW; 77EFF2E874C60B31 CRC64;	ent Scores: No.: 1.08e-29 Length:	Score: 369.00 Matches: 79 Percent Similarity: 77.39% Conservative: 10 Best Local Similarity: 68.70% Mismatches: 18 Query Match: 6 Gaps: 2	US-09-966-880A-7 (1-2818) x Q9BGW3 (1-122)	2151 TICTUTTCTCTCTCTCTTTTTTTTTTTTTTTCTGAGACAGAGTCTTGCTCTTGT	QY 2091 CGCCCAGGCTGGAGTCCAACGCCACGATCTCCAGCTTACTGCAACCTCCACCTCCTGGGTT 2032	Db 24 lGlyGlnAlaGlyValGlnTrpHisAspLeuGlySerLeuGlnProProThrProGlyLe 44 Oy 2031 CAAGCGATTCTCCTGCCTCCAGCTACAGAGTACAGGTGCCTGCTACCAGG 1972
Percent Similarity: 72.65% Conservative: 8 Best Local Similarity: 65.81% Mismatches: 31 Query Match: 7.50% Indels: 1 DB: 4	US-09-966-880A-7 (1-2818) x Q9H387 (1-118)	Qy 2141 CTCTCTCTCTTTTTTTTTTTTTCTCAGACAGACTCTTGCTCTTGTCGCCCAGGCT 2082 ::: ::	2081 GGAGTGCAACGCACGATCTCAGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCC	Db 21 GlyValGinTrpArgAspLeuSerSerProGinProProProProArgPheLysArgPhe 40 Qy 2021 TCTGCCTCAGCTCCCAAGTAGCTGGGATTACAGGTGCCTGCTACCAGCTGGCTAAT 1962	41 SerCysLeuSerProProSerSerTrpAspTyrArgHisAlaProProHisProAlaAsn	<pre>Qy 1961 TTTGCATTTTGACTACAGGGGTTTTGCCAGGCCGGGCTGGTCTCCAAACTCCT 1902 </pre>	Oy 1901 GACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 1842	1841 CCACGCCCGCTCTCTTTTTTTTTTTTTTTTTTTTTTTTT	ThrGlnProAspAlaAsnAsnPheLeuArgLysLeu	RESULT 8	US 1333 ID 09Y555 PRELIMINARY; PRT; 204 AA. AC 09Y555, DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 12, Last annotation update) DF 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DF N15AC2 3 (Pultative novel protein similar to Aborber! Apolitomorptoin B	mRNA editing protein) and Phorbolin) (Fragment). BK150C2.3.		Submitted EMBL; AL(InterPro;	٦.	SEQUENCE	Alignment Scores: 1.09e-29	4 Gaps:	-09-966-880A-7 (1-2818) x Q9Y555 (1-204)	oy inclinación inchemantal contractor de la contractor de	Qy 170 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTCACTGGACTTTGGTTAT 223 :: ::

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75 PheCysAspAspIleLeuSerProAsnThrLysTyrGlnValThrTrpTyrThrSerTrp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC011739; AAH11739.1; -. InterPro: IPR021125; dGMP/Cyt_deam. PROSITE; PS09093; CYT_DCMP_DEAMINASES; UNKNOWN_1. SEQUENCE 190 AA; 22827 WW; DA0584EF75C91CF0 CRC64;
                                                                                                                      GCGTGAGCCACCCCCCCCCTCTCTTTTTTTT 1811
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Similar to APOBEC1.
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134 GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 153
                                                     154 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 173
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Yu Y., Zhang C., Zhou G., Wu S., Qu X., Wei H., Xing G., Dong C.,
Zhai Y., Wan J., Ouyang S., Li L., Zhang S., Zhou K., Zhang Y., Wu
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                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostom1;
Catarrhin1; Hominidae; Homo.
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                                                                                                                174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                   572 CTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
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Tu Y., Gu W., Eu G., Huang C.;
Novel genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIG5520; AAF165501: -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SFOUENCE 294 AA; 33363 MW; 1B39C7A13D690901 CRC64;
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                   2.38e-28
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01-MAR-2002
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TISSUE-TLEAL MUCOSA;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota 'Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Nabo human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AKO00385; BAA91131.1;
SEQUENCE 152 AA; 16568 WW; 59065F45AAA301B5 CRC64;
                                                                                                                                                       Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T. Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK025047; BAB15056.1; -. SEQUENCE 127 AA; 13754 MW; 25851EDBD01EF7F8 CRC64;
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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CDNA: FLJ21394 fis, clone COL03536
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01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
KAIA0536 protein.
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                       Homo sapiens (Human)
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Query Match:
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BE44D01380AD7F6E CRC64;

Hypothetical protein. SEQUENCE 429 AA; 51017 MW;

Alignment Scores:

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                                                  TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT
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174 Ile---LysAsnGlnLeuSerThrSerGluLysLysAlaThrGlyGluSerProValArg
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003114; AAH03114.1;
MGJ; MGJ:193111; BC003314.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 51.0 kDa protein.
BC003314.
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202 IleProValProSerSerSerSerThrLeuSerAsnIleCys-----LeuThr 218
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Matches:
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US-09-265-630-11
US-08-704-711A-1
US-09-521-220-1
US-09-227-357-537
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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US-09-605-785-575
US-09-265-630-13
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US-08-951-200A-1
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                                                                                                                                                                                                                                                                                                     US-08-816-241-5
US-09-040-482-5
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Palo Alto
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Patent No. 5804185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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APPLICATION NUMBER:
FILING DATE:
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STATE: CA
COUNTRY: US
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US-08-816-241-1
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6109.704 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-09-128-395-1

US-08-618-573-121

US-08-454-5576-121

US-08-450-6736-121

PCT-US95-1711A-121

US-09-288-143-168

US-09-288-143-168

US-09-288-143-168

US-08-687-935-1

US-08-687-895-1

US-08-687-895-1
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Patent No. 6087108
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                Indels:
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3174 Porter Drive
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369.50
58.52%
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7.47%
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
           LENGTH: 190 amino acid

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PROSTUT09

CLONE: 1646823
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Best Local Similarity:
Query Match:
DB:
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                                                                                                            Alignment Scores:
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US-08-816-241-1
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Mismatches:
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Matches:
                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                         PF-0239 US
                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/816,241
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BILLIAGS, LUOY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.94e-32
369.50
58.52%
44.89%
7.47%
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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CLONE: 1646823
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                                                                            FILING DATE:
CLASSIFICATION:
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Best Local Similarity:
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1978 TACCACGCCTGGCTAATT -- - TTTGCATTTTGAGTACAGACGGGGTTTTGCCATGTTGGC 1922
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               TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121 CORRESPONDENCE ADDRESS: ADDRESS: STEERET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LeuLeuLeuProArgLeuGluCysAsnGlyAlaIleSerAlaHisArgAsnLeuArgLeu 24
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105 ValSerLeuMetCysProSerTrpSerProGluLeuLysGlnSerThrCysLeuSerLeu
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APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30 MAY-1995
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                       0609.3840003
                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                   NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
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amino acid
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20005-3934
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE BEFERENCE: 210121,427C16
CURRENT APPLICATION NUMBER: 05/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 132
LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
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Matches:
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Patent No. 5830670
GENERAL INFORMATION:
                                                              Sequence 573, Application US/09605785
Patent No. 6321716
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Henderson, Robert A.
Kalos, Michael D.
Fenger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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332.00
71.43%
66.33%
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Skeiky, Yasir A.W.
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Best Local Similarity:
Query Match:
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us-09-966-880a-7.n2p.rai

Page 4

	0y 1880	COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible CORRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CLASSIFICATION NUMBER: US/08/450,673C CLASSIFICATION: 530 ATTORNEY/ACENT INFORMATION: NAME: Ludwig, Steven R: REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.3840004 TELECOMNINICATION INFORMATION: TELECOMNINICATION INFORMATION: TELECOMNINICATION 1NFORMATION: TELECOMNINICATION 1NFORMATION: TELECOMNINICATION 1NFORMATION: TELECOMNINICATION 1NFORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
Qy 1811 TTTTTTTTTTTGAGAGACAGGATCTTGTTATCTTGCCA	195 SULT 5 -08-340-426 sequence 121 atent No. 5 GENERAL INF APPLICANT TITLE OF TITLE OF TITLE OF CORRESPON ADDRESS STREET: CONTRY: STREET: CONTRY ZIP: STREET: CONTRY APPLICAN APPLICAN APPLICAN TELEPHON TELEPHO	Alignment Scores: 1.05e-24 Length: 375 2.05e-24 Length: 375 303.00 Matches: 90 47.14\$ Conservative: 9 47.14\$ Mismatches: 41 1.06e-1.4\$ Indels: 71 6.14\$ Mismatches: 41 6.14\$ Mismatches: 41 6.14\$ Indels: 6 6.14\$ Indels: 1 7.16\$ Indels: 1 8.16\$ Indels: 1 9.16\$ Indels: 1 1.11 Indels: 1 1.11

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Query Match
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Sequence 121, Application PC/TUS9517111A

GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1811 TITITITITITGAGAGACAGGATCTTGTTATGTTGCCCA--
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                                                                                                                     Conservative:
Mismatches:
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Matches:
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303.00
47.14%
42.86%
6.14%
: 375 amino acids
amino acid
                                     ; MOLECULE TYPE: protein US-08-450-673C-121
                             linear
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                                                                                                                                Similarity:
                                                                                                              Percent Similarity:
Best Local Similari
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                        TOPOLOGY:
 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 uSerLeuProSerSerTrpAspTyr-GlyHisLeuHisHisThrProLeuIlePheValP 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397
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                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                  NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/17111A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 22, Application US/09058489; Patent No. 6103886; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                               MEDIUM TYPE: Floppy disk
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295.00
66.67%
57.50%
5.98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 397 amino acids TYPE: amino acid
                     COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
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Best Local Similarity:
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EARLIER FILING DATE: 1997-10-09
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TrpArgCysGluSerAsnArgSerHisThrThrIleAlaLysTyrAlaGlnTyrGlnAla
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Matches:
Conservative:
Mismatches:
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Petent No. 6433139
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REPERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER PILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
               TILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER PELICATION NUMBER: 60/041,877
EARLIER PILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 1079
TYPE: PRT
USGANISM: Human
US-09-058-489-22
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TITLE OF INVENTION: the Y Chromosome
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287.00
61.54%
53.15%
5.81%
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Best Local Similarity:
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Mismatches:
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Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER PLING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER PILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PALENTIN VET. 2.0
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,732
FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
FILING DATE: 1997-07-08
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286.00
71.88%
65.62%
5.79%
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US-09-288-143-168
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Best Local Similarity:
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2066 GATCTCAGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTC 2007
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Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INFORTION:
NUMBER OF SEQUENCES: 5
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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271.00
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MEDIUM TYPE: Diskette
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CLONE: 57953
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Matches:
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NAME/KEY: SITE
LOCATION: (110)
OTHER INFORMATION: Xea equals stop translation
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APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/055,948
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,949
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,953
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EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver: 2.0
                                                                                    FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,920
FILING DATE: 1997-07-08
                                                                                                                                        APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,795
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FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-09-12
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FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
APPLICATION NUMBER: 60/051,916
                                 APPLICATION NUMBER: 60/051,930
                                                                       APPLICATION NUMBER: 60/051,918
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APPLICATION NUMBER: 60/055,984
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                                                    FILING DATE: 1997-07-08
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                1997-07-08
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5.63%
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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|S1 ValGlyArgLeuPheMetTrpGlu------GluProGluIleGlnAlaAlaLeu 166
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92 AspGluHisAlaAlaHisAlaGluGluAlaPhePheAsnThrIleLeuPro---Ala
                              TACGIAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC
                                                        TyrvalValGluAlaGlnGlyLysGlyGlyGlnValGlnAlaSerArgGlyTyrLeuGlu
                                                                                              AATAAGAAC---GGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGAC
                                                                                                                                                              CTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: CA
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
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APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09040482
Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AspGluHisAlaAlaAlaHisAlaGluGluAlaPhePheAsnThrIleLeuPro---Ala 110
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Patent No. 634281
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                                                                                                                US-09-966-880A-7 (1-2818) x US-09-040-482-1 (1-222)
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Indels:
                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                            271.00
50.00%
35.80%
5.48%
                 TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
  single
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Best Local Similarity:
STRANDEDNESS:
                                                                                                    ; CLONE: 57953
US-09-040-482-1
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US-09-227-357-285
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Conservative:
Mismatches:
Indels:
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Matches:
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-09-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APP
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5.02%
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
US-09-227-357-285
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Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 122
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1874 CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCTCTCTTTTT 1815
                          1934 TIGCCATGTIGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGC 1875
                                                                                         1994 GATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTACAGACGGGGTT 1935
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
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Conservative:
Mismatches:
Indels:
US-09-966-880A-7 (1-2818) x US-09-227-357-285 (1-122)
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTONNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08687895 Patent No. 5747319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
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245.00
61.82%
46.36%
4.95%
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OPERATING SYSTEM: DOS
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US-08-687-895-3
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Best Local Similarity:
Query Match:
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                                                                                                            119 TACTICIGIGAGGACCGCAAGGCIGAGCCC-----GAGGGGCIGCGGCGGCGCTGCAC 469
                                                                                                                                                                                                                                          170 CGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACT 529
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82 PheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGln 101
                                                              305 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
           US-09-966-880A-7 (1-2818) x US-08-687-895-3 (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
ACMRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                        590 CGTCTCTCCAGACAGCTTCGGCGCATCCTT 619
                                                                                                                                                                                                                                                                                                                                                                                          NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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; CLONE: 436941
US-08-816-241-3
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CITY: Palo Alto
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305 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT 358
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82 PheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGln 101
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                              Conservative:
Mismatches:
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Sequence 1639, App Sequence 1639, Ap

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Sequence 105, App
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Sequence 237, App
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Sequence 198, App
Sequence 282, App
Sequence 282, App
Sequence 573, App
Sequence 884, App
Sequence 190, App
Sequence 190, App
Sequence 157, App
Sequence 157, App
Sequence 154, App
Sequence 157, App
Sequence 27, App
               US-09-925-300-1639
US-09-989-919-105
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US-09-989-920-233
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US-10-082-830-207
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US-09-989-920-198
US-09-986-981
US-09-986-480-282
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US-10-19-995-494-79
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US-09-764-891-5337
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US-10-001-858-154
US-10-001-858-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Muramatsu, Masamichi
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 1090-03-28
PRIOR FILING DATE: 1990-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09966880A; Patent No. US20020164743A1; GENERAL INFORMATION:
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LENGTH: 198
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                                       Sequence 8, Appli
Sequence 2, Appli
Sequence 174, App
Sequence 193, App
                                                                                                                                             (without alignments)
6641.044 Million cell updates/sec
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                                                                                                                                                                                                                                    Description
                                                                                                                        June 14, 2003, 18:26:00 ; Search time 90.7352 Seconds
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-966-880A-2
0 US-09-729-674-174
0 US-09-800-729-193

    protein search, using frame_plus_n2p model

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Length:
Matches:
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APPLICANT: HONJO, TRSUKU
APPLICANT: HONJO, TRSUKU
APPLICANT: HONJO, TRSUKU
TITLE OF INVENTION: NOVEL CYTDINE DEAMINASE
FILE REFERENCE: 06501-08801
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DCT/TP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR PILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR PILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 2
TYPE: PRI
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Patent No. US20020164743Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620 TICCCCCTGIAIGAGGIIGAIGACTIACGAGACGCATITCGIACTIIGGGA 670
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Matches:
Conservative:
Mismatches:
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                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacoby, Kenneth
APPLICANT: Jacoby, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Warberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Gallinger II, Robert J.
APPLICANT: Gallinger II, Robert J.
APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 174, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
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Steininger II, Robert J.
Spaulding, Vikki
1.51e-94
1008.00
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92.89%
                       Percent Similarity:
Best Local Similarity:
Query Match:
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1913 TCTCAAACTCCTGACCACAGGTGATCCGCCCGGCTCGGCCTCCCAAAGTGCTGGGATTAC 1854
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APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                    US-09-966-880A-7 (1-2818) x US-09-800-729-193 (1-239)
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Indels:
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Matches:
      PCT/US00/26013
   PRIOR APPLICATION NUMBER: PCT/US00/20
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver: 2.0
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; Patent No. US20020068319A1
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SOFTWARE: PatentIn Ver.
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US-09-800-729-193
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LENGTH: 239
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LENGTH: 310
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APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFRENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: 984
; LENGTH: 384
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Patent No. US20020068319A1
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Best Local Similarity:
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Pred. No.: 4.5e-30 Length: 310 Score: 381.50 Matches: 87 Percent Similarity: 72.39% Conservative: 10	Query Match: 7.73	178 PheserPheLeuserPhePhePhePhePhePhePhePhePheLeuArgIrgCTCTGGGGGCTCTTGCTTTTTTTTTTTTTTTTTTTTGGGGGG	Db 217 ySerSerAsnSerPtroAlaLeuAlaSerGlnValAlaGlyIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1853 AGCGTGAGCCACCACGCCGGCCTCTCTCTTTCTT 1817 Db 277 eGlyValSerHisArgAlaArgProGlySerValPheLeu 290 RESULT 6	Sequence 1639 Application US/09925300 Sequence 1639 Application US/09925300 Sequence 1639 Replication US/099	; CURRENT FILING DATE: US/09/925,300 ; PRIOR APPLICATION NUMBER: PCT/USO0/05988 ; PRIOR FILING DATE: 2001-08-10 ; PRIOR PILING DATE: 2000-03-08 ; PRIOR APPLICATION NUMBER: 60/124,270 ; NUMBER OF SEQ ID NOS: 1890 ; SOFTWARE: PatentIn Ver. 2.0 ; ELNGTH: 222 ; TYPE: PRT ; ORGANISM: Homo Sapiens	Alignment Scores: Pred. No.: Score: Score: Pered. Sinilarity: Best Local Similarity: Best Local Similarity: A4.89% Mismatches: 10 Gaps: US-09-966-880A-7 (1-2818) x US-010-975-200-1620	

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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 233
LENGTH: 107
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| Publication No. US20030039986A1
| GENERAL INFORMATION:
| APPLICANT: Sun, Yongming | APPLICANT: Chen, Sel-Yu | APPLICANT: Chen, Sel-Yu | APPLICANT: Liu, Chenghua | APPLICANT: Liu, Chenghua | TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific | TITLE OF INVENTION: Genes and Proteins
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CURRENT APPLICATION NUMBER: US/10/011,585A
CURRENT FILING DATE: 2002-03-14
                                         Sequence 233, Application US/09989920
Patent No. US20020172957A1
GENERAL INFORMATION:
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                              09-989-920-233
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Sequence 135, Application US/10001835

Parent No. US2002016038741

GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TILLE OF INFORMITON: Compositions and Methods Relating to Ovary Specific Genes and Prc
TILLE REFERENCE: DEX-0277
CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT APPLICATION NUMBER: US/10/01-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 135
LENGTH: 94
LENGTH: 94
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Matches:
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Mismatches:
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Best Local Similarity:
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-----TTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGA 2065
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                                                                                                                                                                                                                                                                                                                      2006 CCAAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGT 1947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0249
CURRENT APPLICATION NUMBER: US/10/082,830
CURRENT APPLICATION NUMBER: 60/243,802
PRIOR APPLICATION NUMBER: 60/243,802
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 282
                                                                                                                                                                                                                                                                        4 PhePhePheSerLeuArgGlnSerLeuThr-LeuSerProArgLeuGluCysSerGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                1886 GCCCGCCTCGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCAC 1838
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                                                                                Conservative:
Mismatches:
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Mismatches:
                                                  Length:
Matches:
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Matches:
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                                                                                                                                 Gaps:
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                                   7.32e-28
358.00
85.578
75.26%
7.25%
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351.50
72.50%
64.17%
7.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens US-10-082-830-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                 Percent Similarity:
Best Local Similarity:
   JS-10-016-157A-171
                                     Alignment Scores:
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Sequence 171, Application US/10016157A

Publication No. US20020192220A1

GENERAL INFORMATION:

APPLICANT: Secipon, Herve
APPLICANT: Ghosh, Malavika
APPLICANT: Ghosh, Malavika
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Profile Compositions and Methods Relating to Colon Specific Genes and Profile Composition NUMBER: US/10/016,157A

CURRENT FILING DATE: 2001-10-31

CURRENT FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 250

SEQ ID NO 171

LENGTH: 100
                                                                                                                                                                                                                                                                                                                  2263 ACAAATAGACACCAAAAGAGACAAATAGGG-----ATCCTTATTGGCTCCTTACATTT 2210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ------SerPhePhePhePhePhePheLeuArgGlnSerPheThrLeuLeu- 52
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Mismatches:
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PRIOR APPLICATION NUMBER: 60/245,740 PRIOR FILING DATE: 2000-11-03 NUMBER OF SEQ ID NOS: 245 SOFWARE: Patentin Ver. 2.1 SEQ ID NO 145
                                                                                                                                                                        6.72e-28
359.00
68.42%
56.58%
                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-585A-145
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ORGANISM: Homo sapiens
                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Cher, Sel-Yu
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and is
FILE REPERENCE: DEX-0291
FILE REPERENCE: DEX-0201
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SSPTWARE: PatentIn version 3.1
SEQ ID NO 198
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2119 TTTTTCTGAGACAGAGTCTTGCTCTTGTCGCCCAGGCTGGAGTGCAACGGCACGATCTCA 2060
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PUblication No. US200300279941
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/134,068
PRIOR APPLICATION NUMBER: US 60/134,068
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
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Mismatches:
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349.50
68.46%
60.00%
7.08%
                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-920-198
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Best Local Similarity:
Query Match:
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                            2004 AAGTAGCTGGGATTACAGGTGCCTGCTACCACGCCTGGCTAATTTTTGCATTTTGAGTAC 1945
                                                                                                                                                                   1944 AGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCACAGGTGATCCGC 1885
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                                                                                                                                                                                     21 LysLeuArgLeuProGlySerSerAspSerProThrSerAlaSerGlnValAlaGlyIle 40
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                                                                                                                                                                                                                                   1884 CCGGCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCC 1829
                                                                                                                                                                                                                                                    Sequence 1058, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
FILO APPLICATION ADDIESTOR OF SEQ. 100.01-17
PLIOR APPLICATION ADDIESTOR OF SEQ. 100.05: 1792
SOFTWARE: PATENTING VET. 2.0
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Matches:
Conservative:
Mismatches:
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351.00
80.00%
72.63%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-764-864-1058
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Best Local Similarity:
Query Match:
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LENGTH: 172
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2233 ATCCCTTATTGGCTCCTTACATTTTGTTGGATAAAGCACAATTTCCTTGCAATGCTTCCC 2174
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                                      PEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (173)
NAME/KEY: SITE
LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2053 TGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGG 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LOCATION: (186)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-986-480-433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TrpPro-ProArgL 153
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                                                                                                                                                                                                                                                                           198
86
17
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                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	AB040431 AB040431 Homo sapi	ABO40430 HOMO S AC092184 HOMO S	ВС006296 Ношо sap		AF529815 Homo sap	AF529816 HOMO	AF529819 HOMO	AF529820 HOMO AF529821 HOMO	AF529822 HOMO	AF529823	AF529825 HOMO	AF529826 HOMO	AF529827 HOMO AF529829 Mus	AF529830 Mus	AF529831 AF529833	AF529835 Mus mus	AF529837 Mus	AF529834	AF529817 HOMO	AF529818 Homo	AF529832 Mus AF529836 Mus	AF529838	AF529841	AF529842	. AF529843	AF529845	AF529846		AF529849	AF529850	AF529851	AF329832 AF530853	AF529854	AF529855 Cricetul	ALIGNMENTS		2791 bp mRNA linear PRI 03-OCT-2000 for activation-induced cytidine deaminase,		cytidine deaminase; Human AID.	MKNA.	Chordata; Cranlata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.		and chromosomal
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                                                                                                                                                     Direct Submission
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku,
Kyoto, Kyoto 606-68501, Japan (E-mail:honjo@mfour.med.kyoto-u.ac.jp,
Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388)
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QQ		qa	10090 GTTCAAGGCCAGCCTGC
δy	3TCCTTCAAGTCTTCTCTGTTTTTATTCTTCAACTCTCACTTTCTTAGAGTTTACA	Qy	1817 AAGAAAGAGAGGGCC
QQ	91	q _Q	10150 AAGAAAGAGAGAG
οy	856	οy	1877 CGAGCCGGGCGGATCAC
ą		qq	10210 CGAGCCGGGCGAT
Qy	FICTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGCAACATTGTCCCCTA 916	QY	1937 CCCCGTCTGTACTCAAA
q	~ ~	qq	10270 ccccgrcrgrAcrc
Οy	SAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTCAACGTTTTTTTT	οy	1997 AGCTACTTGGGAGGCTG
q	3	qq	10330 AGCTACTTGGGAGG
٥y	103	δλ	2057 AGCTGAGATCGTGCCGT
qq	9310 CTTTTAGGTAGGATGAGAGCAGAAGGTAGATCTAAAAAGCATGGTGGAGGATCAAATG 9369	qq	0
Qy	1037 TITITATATCAACATCCTTTATTATTTGATTCATTTGAGTTAACAGTGGTGTTAGTGATA 1096	ΟŸ	,
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٥y	1157 CCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTC 1216	δy	2237 TATTTGTCTCTTTTGGT
ΩÞ	9490 CCATGATCTATAGGACCTCCTAATGAGAGTATCTGGGTGATTGTGACCCCAAACCATCTC 9549	qa	0
ογ	1217 TCCAAAGCATTAATATCCAATCATGCGCTGTATGTTTTAATCAGCAGGAAGCATGTTTTA 1276	οy	6
Dp	9550 TCCAAAGCATTAATATCCAATCATGCGTGTATGTTTTAATCAGCAGAAGCATGTTTTA 9609	Q O	30
ογ	1277 IGTITGIACAAAAGAAGGITGITAIGGGGGGGGGAGGGAATAGGCCATGCAIGGICAC 1336	ογ ,	5
qq	9610 TGTTTGTACAAAAGATGTTATGGGTGGGGATGGAGGTATAGACCATGCATG	Q O	069
Οy	1337 CTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGTGAACAAGACCCC 1396	Oy.	17
QQ	9670 CTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACTGTGAACAAGACACCC 9729	QQ ·	750 TGTA
οy	1397 TAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAA 1456	δy	
QQ	9730 TAATAATGGGTTGATGTCTGAAGTAGCAAATCTTCTGGAAACGCAAACTCTTTTAAGGAA 9789	qq	810 CTAA
Qy	1457 GTCCCTAATTTAGAAACACCCACAAACTTCACATATCATAATTAGGAAACAATTGGAAGG 1516	Οy	_
qq	9790 GTCCCTAATTIAGAAACACCCACAAACTTCACATATTAGCAAAACAATAGGAAATTGGAAGG 9849	qq	870 T
Qy	157	Qy	2597 AGTAATGGTGCTACGAA(
qq	9850 AAGITGCIICAAIGITGGGGAGAAGAAAATCIAITGCICTCGGGGGTCTCIICAICIA 9909	qq	930 AGTAATGGTC
Qy	1577 GAAATGCCAATCAGGTTTGCTACATTTTGTATGTGTGTGT	Ολ	2
οp		qa	06
οy	1637 GTATATTAACTATAAAGAGAGTTGTGACAAAACAGAATGATAAAGCTGCGAACCGTGGC 1696	Οy	2717 ATAAAATACCAAATAAA
qq		qa	020
Qy	1697 ACACGCTCATAGTTCTAGCTGCTTGGGAGGTTGAGGAGGAGGATGGCTTGAACACAGGT 1756	Ολ	2777 TATGATGGAATAAACTTC
qq		qq	11110 TATGATGAATAAA

CCGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC CCCTGTGCCGTTATTACCTAGCAACCCTTGCAATGAAGATGAGC **AAATGCAAAAATTAGCCAGGCGTGGTAGCAGGCACCTGTAATCCC** AACATGATTTCCTTTTCTGATATTGAAATGGAGTCTCAAAGC FITGCACTCCAGCCTGGGCGACAAGAGCAAGACTCTGTCTCAGAA GAGAGAGAGAAAAGAGAACAATATTTGGGAGAGAAGGATGGGG TTGTGCTTTATCCAACAAATGTAAGGAGCCAATAAGGGATCCC TTGAATGCACAACTGTCTTATTTAATCTTATTGTACATAAGTT **ATTGTTACTTCATGTATTCATTTATATTTTATATTTTGCGT** | CAATCAGTTAAATAAATGATAAATAATTTTGGAAGCTGTGAAG ||| | |GAGA 11130 FGAAA 2797

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/rpt_family="AluSq"
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4 (Davie, S. Davie, S. Davie, S. Davie, S. Davie, D. Davie, S. Catron, T. Parametr, C. Davie, C. Caron, T. Davie, C. Caron, T. Davie, C. Caron, D. Chocko, J. Chavez, D. Cheveland, C. D. Cox, C. Coyle, M. D. Dathorne, S. R. David, R. Davie, C. D
                                Homo sapiens 12 BAC RP11-438L7 (Roswell Park Cancer Institute Human AC09184 AC09184 AC013443
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                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inocal mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 71132)
Worley, K.C.
Direct Submission

Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA (DAY 25, 2002 this sequence version replaced gi:20901754.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
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complement(1. .1448)
/note="overlaps bases 1. .1448 of clone AC092490"
/function="clone overlap"
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/standard_name="57233"
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774. .881
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1744. .1819
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1591. .1807
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1191. .1213
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903. .1190
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SOURCE Homo sapiens. ORGANISM Homo sapiens. Brokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Brokaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. I (bases I to 1837) Strausbarg R. TITLE Direct Submission Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov CONMENT Email: cgapbs-r@mail.nih.gov CONMENT Sequencing Dy: National Institutes of Health Intramural Sequencing Dy: National Institutes of Health Intramural Sequencing Dy: National Institutes of Health Intramural Sequencing Contact: National Institutes of Benishins, B. Blakesley, R.W. Bouffard, G.G., Brinkley, C., Brooks, S., Bletrich, N.L., Guana, X., Guptea, J., Ho, SL., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastrian, S.D., McCloskey, J.C., Lim, M., Maduro, C., Mastrian, S.D., McCloskey, J., C., C., McCloskey, J., C., C., McCloskey, J., C., McCloskey, J., C., McCloskey, J., C., C., McCloskey, J., C., McCloskey, J., C., C., C., C., C., C., C., C., C., C	Tiongson, E. E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, LH. and Green, E.D. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: IT Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9988409. Location/Qualifiers Location/Qualifiers //db_xref="LocusiD:57379" //db_xref="LocusiD:57379" //clone="MGC:12911 IMAGE:4054915"	/tissue_type="primary B-cells from Tonsils" /clone_lib="NHH_MGC_48" /lab_host="Lh10B-R" /note="vector: poTB7" 86. 682 /codon_stert=1 /product="activation-induced cytidine deaminase" /protein_id="AAH06296.1" /protein_id="AAH06296.1" /db_xref="GI:13623401" /db_xref="GI:13623401" /translation-imDSLLMNRKFLYQFKNVFWAKGRRETYLCYVVKRRDSATSFSL /translation-imDSLLMNRKFLYGFKNVFWAKGRRETYLCYVVKRRDSATSFSL /translation-imDSLLMNRKFLYGFKNVFWAKGRRETYLCYVVKRRDSATSFSL /ranslation-imDSLLMNRKFLYGFKNVFWAKGRNAFFKNNF /db_xref="GI:13623401" /db_xref="GI:1462401" /db_xref="GI:1462401" /db_xref="GI:14623401" /db_xref="GI:1462401" /db_xref="GI:1462401	Query Match 64.6%; Score 1820; DB 9; Length 1837; Best Local Similarity 99.7%; Pred. No. 0; No. 0; Adstractive 0; Gaps 0; Qy 1 AGAGAACCATCATTAATTGAAGTGAGATTTTTCTGGCCTGAGACTTGCAGGAGGCAAGA 60 1	Qy 61 AGACACTGGACACCACTATGGACAGCTCTTGATGAACCGGAGGAAGTTCTTTACCA 120 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
0y 1877 CGAGCCGGCGGATCACCTGTGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAA 1936 11 111111111111111111111111111111111111	Qy 2297 TTCAGAATAACCATATCCTGTGCAACCTTGCAATGAAGATGAGC 2356 bb 45173 TTCAGAATAACCATATCCTGTGCCGTTATTACCTAGCAACCATGAAGATGAGC 45232 Qy 2357 AGATCCACAGGAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTT 2416 Db 45233 AGATCCACAGGAAAACTTGAATGCACAACTGTCTTATTTTAATCTTATTGTACATAAGTT 45292 Qy 2417 TGTAAAAGAGTTAAAAAATTGTTACATCATGTATTTTAATCTTATTTTGCGT 2476 Db 45293 TGTAAAAAGAGTTAAAAAATTGTTACTTCATGTATTTTATTTTTATTTTTGCGT 45352 Qy 2477 CTAAAAAGAGTTAAAAAATTGTTACTTCATGTATTTTATATTTTTTTT	45353 CTAATGATTTTTATAACATGATTTCCTTTTCTGATATATGAAATGGAGTCTCAAGG 2537 TTCATAAATTTTATAACATGATTTCCTTTTCTGATATATGAAATGGAGTCTCAAGG 2537 TTCATAAATTTATAACATGATTTCCTTTTCTGATATTGAAATGGAGTCTCAAGG 2537 TTCATAAATTTATAACTTTAGAAATGATTCTAATAACAACGTATGTAATTGTAACATTGC 2597 AGTAATGGTGCTACGAAGCCATTTCTCTTGATTTTAGTAAACTTTTATGAACATTGC 2597 AGTAATGGTGCTACGAAGCCATTTCTCTTGATTTTTTTTAGTAAACTTTTATGAAGCAAATT 2597 AGTAATGGTGCTACGAAGCCATTTCTCTTGATTTTTTAGTAAACTTTTTTTT	Oy 2717 ATAAATACCAAATAAAATAATAAAAGTGATTTATATGAAGTTAAAATAAAAAA	RESULT 4 BC006296 LOCUS BC006296 LOCUS BC006296 BC106296 ACCESSION BC006296 ACCESSION BC006296 VERSION BC006296 ACCESSION BC006296 VERSION BC006296 ACCESSION BC006296 VERSION BC006296 ACCESSION BC006296

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                                                                                                                                       ACCATGCATGGTCACCTTCAAGCTACTTTAATAAAGGATCTTAAAATGGGCAGGAGGACT
                                                                                                                                                                     GTGGTGTTAGTGATAGATTTTCTATTCTTTTCCTTGACGTTTACTTTCAAGTAACACA
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                                                    TGAGAGGATCAAATGTTTTATATCAACATCCTTTATTATTTGATTCATTTGAGTTAACA
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<u> AATAGAGAAGGAACACAGGTCTGGCCAGGGACGTGCTGCAATTGGTGCAGTTTTGAATGC</u>
                                         AACATTGTCCCCTACT-GGGAATAACAGAACTGCAGGACCTGGGAGCATCCTAAAGTGTC
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/db_xref="taxon:10090"
/clone="1"
/cell_type="hybridoma Pl-5"
/transgenic
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Direct Submission
Submitted (17-7UL-2002) Cell Biolo
Medicine, 1300 Morris Park Ave. Ch
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Eukaryota; Metazoa; Chordata; Cl
Mammalia; Eutheria; Rodentia; St
1 (bases 1 to 597)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AII
Unpublished
2 (bases 1 to 597)
                    AGGACCGCCAGAGCAATGATGTAAC-
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                          /product="activation-induced cytidine deaminase"
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MWGGLHBNSVRLTROFRRILLPLXEVDDLRDAFRMLGF"
546 c 551 g 636 t 1 others
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Pred. No. 1.2e-108;
0; Mismatches 351;
          /note="APOBEC-1 homologue"
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llarity 69.4%;
Conservative
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Matches 1006; Conser
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NLSLRIFTARLYFCEDRRAFERGLRFLHRAGVOIAIMTFKDYFYCWNTFVENHERTFR
AWEGLHENSVRLSRQIRRILLPLYEVDDLRDAFRTLGL
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0
                                                    Unpublished
2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-310-2002) Cell Biology, Albert Einstein (Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
                                           cells
         Hominidae;
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                                        AID transgene in
       Catarrhin1;
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Pred. No. 6.5e-107
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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       Eutheria; Primates;
1 to 596)
                      Scharff,M.D.
mutation of the
                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                     /note="integrated
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                                       Somatic hypermutation
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Martin, A. and S
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                                                                                         /product."AlD"

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PGTJRRNNDHVBLLELRYXTSDWBLDPGRQYRVWTTSWSPCYDCRRHVADFLRGNP
NLSLRIFTARLYFCRDRAREPEGLRLHAAVQIAIMTFKDYFYCWNTFVENHERTFR

AWGGLHENSVRLSRQLRRILLPLYFVDDLRDAFRTIGL"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                        Score 595.4; DB 12;
Pred. No. 4.1e-107;
0; Mismatches 1;
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      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                               /codon_start=1
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                                       /gene="AID"
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al Similarity 99.8%;
596; Conservative
                                                                   /gene="AID"
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/translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
DRGYLRNKWGCHVELLELRYX LSDWDLDDGRCKYRVTWFTSWSPCYDCARHYADFLRGNP
DLSLAFTARLYFCBHKAREPGLRELHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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Submitted (17-701-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
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                GCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGGGGTGCAAATAGCCATCATGACC
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Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
/clone="Ramos 5"
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/db_xref="GI:22297226"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Martin, A. and Scharff, M.D.
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AF529819
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Homo sapiens clone Ramos 2 AID (AID) mRNA, partial cds.
AF'529816
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                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 596)
2 (bases 1 to 596)
Burtin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
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Catarrhini; Hominidae; Homo.
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/db_xref="GI:22297220"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Martin,A. and Scharff,M.D
Somatic hypermutation of
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Martin,A. and Scharff,M.D.
Direct Submission
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
1. .596
//organism="Homo sapiens"
//db.xref="texon:9606"
1. .>596
                                                                        ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: E
Mammalia: Eutheria: Primates: Catarrhini: Hominidae:
I toases: 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells
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7 AID (AID) mRNA,
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                             DB
                           Score 594.4; I
Pred. No. 6.5e-
0; Mismatches
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NLSLRIFTARLYFCVDRRAEPEGLRLHRAGYQIALWTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSROLRRILLPLYEVDDLRDAFRTLGL"

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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG
                                                                                                AACCCCAACTCAGTCTGAGGATCTTCACCGCGCCTCTACTTCTGTGAGGACCGCAAG
                                  TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
                                               Marin, A. and Scharff, M.D. Somatic hypermutation of the AID transgene in B cells and non-B
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Catarrhini; Hominidae;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 6"
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1 (bases 1 to 596)
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//protein_id="ADSLDAMPREDIA"
//protein_id="MoslLAMPREDIA"
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2 (bases 1 to 596)
Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
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Mammalia; Eutheria; Primates;
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the
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- 163 c 155 g 150 t
                 PRI 19-AUG-2002
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College and Submitted (17-JUL-2002) Cell Biology, Albert Einstein College Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Catarrhini; Hominidae;
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Pred. No. 6.5e-107;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="Ramos 9"
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Mammalia; Eutheria; Primates;
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                        Homo sapiens clone Ramos
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AWEGLHENSVRLSRQLBRILLEDLYEVDDLRDAFFLGGL
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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/product-"AID"
/db_xref-"di-"AAM95412.1"
/db_xref-"di-"2297238"
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NLSLRIFTARLYFCEDRRAEPEGLRRLHRAGYQIAIMTFKDYFYCWNTFVENHERTFK
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
1. 596
/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkitt's lymphoma cell line
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Catarrhini; Hominidae;
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Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B
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No. 6.5e-107;
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11 AID
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1. >596
/gene="AID"
/note="integrated into
                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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AF529825.1 GI:22297237
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99.8%;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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AF529825
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11397.322 Million cell updates/sec
                                         June 18, 2003, 23:33:05 ; Search time 1524.43 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                         2054640 seqs, 14551402878 residues
                                                                      US-09-966-880A-7_COPY_80_676
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Maximum Match 100%
Listing first 45 summaries
                           - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1837)
Strausberg, R.
Direct Submission score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AB040431 Homo s AF529828 Mus n AF529815 Homo s ВС006296 Ното Description ALIGNMENTS SUMMARIES AF529816
AF529819
AF529820
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AF529824
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AF529826
AF529826
AF529830 AF529834 AF529817 AF529818 AF529832 AF529831 AF529833 AF529835 AF529837 AF529836 AF529842 AF529815 BC006296 BC006296.1 GI:13623400 DB Length Homo sapiens. Query Match MGC Score 594.4 594.4 594.4 ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

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and Durandy, A.
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NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,P., Legaspl.R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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Submitted (09-APR-2001) National Institutes of Health, Mammalian
                   Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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CODA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site:
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/organism="Homo sapiens"
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/tissue type="Primary B-Cells from Tonsils"
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/note="Vector: pOTB7"
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                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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NLSLRTFTARLYFCDBRRAEPEGLREHHRAGYOIAIWFRDYFYCWNTFVENHERTFR
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens AID mRNA for activation-induced cytidine deaminase, complete CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 597
AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
                           GCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACC
                                                                                                                                                                                                                                                                                                                                                         GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
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Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T. Isolation, Lissue distribution, and chromosomal localization human activation-induced cytidine deaminase (AID) gene Genomics 68 (1), 85-88 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Revy, P., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O. Catalan, N., Forveille, M., Dufourcq-Lagelouse, R., Gennery, A., Tezcan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brousse, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activation induced cytidine deaminase (AID) deficiency cause autosomal recessive form of the Hyper-IgM syndrome (HIGM2) cell 102 (5), 565-575 (2000)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens cDNA to mRNA.
Homo sapiens
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77 673
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us-09-966-880a-7_copy_80_676.rge

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AWEGLHENSVRLSRQLRRILLDLYEVDDLRDAFRTLGL"
164 c 154 g 150 t
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                                                                                                                                                                                                                                              Length 597;
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partial
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Pred. No. 7e-150;
0; Mismatches 1; Indels
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         cell_type="hybridoma Pl-5"
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1 AID (
                                                    /db_xref="taxon:9606"
1. 597
/gene="AID"
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Homo sapiens clone Ramos
AF529815
AF529815.1 GI:22297217
                                            /organism="Homo
                                                                                                                   /codon_start=1
                                                                                                                            /product-"AID"
                                                                                                                                                                                                                                            / Match 99.7%;
Local Similarity 99.8%;
nes 596; Conservative (
                         /transgenic
                                                                                                     /gene="AID"
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Sciurognathi; Muridae; Murinae; Mus
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Direct Submission
Submitted (17-J002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            673
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                                 Score 597; DB 9; 1
Pred. No. 3.3e-150;
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                                                       Mismatches
176
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Mammalla; Eutheria; Rodentia; Sc
1 (bases 1 to 597)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID
Unpublished
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 625
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                                Similarity 100.0%;
7; Conservative C
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Fri

PRI 19-AUG-2002

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Euteleostom1;

cells and non-B

of USA

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/product="AlD"
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/protein_id="AAM95403.1"
/protein_id="AAM95403.1"
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NLSLRIFFRARLYFCEDRKAEPEGLRRLHRAGVQIAIWTFKDYFYCWNTFVENHERFFFR
AWGGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"

165 c 155 g 149 t
              /note="integrated into Burkitt's lymphoma cell line Ramos"
/codon_start=1
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                              Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 594.4; DB 9;
99.8%; Pred. No. 1.3e-149;
iive 0; Mismatches 1;
                                                                                                                               MRNA
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                              596 bp
2 AID (
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                                                                                                                                                                                                                         Eutheria; Primates;
                                                                                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Direct Submission
                                                                                                                         AF529816
Homo sapiens clone Ramos
AF529816
AF529816.1 GI:22297219
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Ramos 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AID"
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/qene="AID"
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es 595; Conserv
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/codon_start=1
/codon_start=1
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NLSLRIFTARLYFCEDRKAEPEGLERRLHRAGYQIAINTFKDYFYCWNTFVENHERTFK
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Catarrhini; Hominidae; Homo.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-2002) Cell Biology, Albert Einstein College Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Pred. No. 1.3e-149;
0; Mismatches 1;
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/clone="Ramos 1"
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Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
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Martin,A. and Scharff,M.D.
Somatic hypermutation of the Al
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/translation="MOSLLMNRRKFLYQFKNVRWAKGRETYLCYVVKRRDSATSFSL
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NLSLRIFTARLYFCVDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFR
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Catarrhini; Hominidae; Homo.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted To JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="GI:22297228"
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/d_xxef="cd::22297226"
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Submitted (17-JUL-2002) Cell Biology, Albert Einstein
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="Ramos 5"
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Somatic hypermutation of the AID
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Martin, A. and Scharff, M.D.
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College (
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U.
Location/Qualifiers
                                                              Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 596)
Martin,A. and Scharff.M.D.
Somatic hypermutation of the AID transgene in B cells and
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AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
| 164 c 155 g 151 t
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7 AID (AID) mRNA,
                                       Score 594.4; DB 9;
Pred. No. 1.3e-149;
0; Mismatches 1;
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Pred. No. 1.3e-149;
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8 AID (
'db_xref~"taxon:9606"
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AF529822
                                                                              /codon_start-1
                                                                                          /product-"AID"
             /clone="Ramos
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                               /gene="AID"
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/protein_id="AAM95410.1"
/db_xref="G1:22297234"
/translation="MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSL
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NLSLAIFTRARLYRCEDRKAEPEGLRRLHRAGYQIAINTFKDYFYCWNTFVENHERTFK
AMEGLHENSYRLSRQLRRLLLELYFYDDLRDAFRTLGL"
163 g 150 t
                                                                              596 bp mRNA linear PRI 19-AUG-2002
9 AID (AID) mRNA, partial cds.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, US Location/Qualifiers
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Catarrhini; Hominidae;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 9"
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                                                                                                                                                                       Chordata; Primates;
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                                                                                       Homo sapiens clone Ramos AF529823
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DRGYLRNKNGGHVELLELRY ISDWDLDGGRCYRUWFFSWSPCYDCARHYADFLKGNP
DRSLR IFTARLYFCBRRAPEGLREHRAGYQIAIWFFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRTLGL"
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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/db_xref="GI:22297232"
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
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Martin,A. and Scharff,M.
Somatic hypermutation of
                                                                                GI:22297245
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                                                                                                           Mus musculus
Eukaryota; Metazoa;
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Local Similarity 99.8%;
les 595; Conservative
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DEGYLARKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRFIARLYFCEDRKAEPEGLRRUHRAGYQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSGRRILLPFYDDLRDAFRTLGL"
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Martin, A and Scharff, M.D.
Direct Submitted (I7-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
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  Somatic hypermutation of the AID transgene cells
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Pred. No. 1.3e-149;
0; Mismatches 1;
                                                                                               /organism="Homo sapiens"
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-07-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers 1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGG Murinae; TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCCGACATGTGGCCGACTTTCTGCGAGGG Gaps and non-B ; 0 Cranlata; Vertebrata; E Sciurognathi; Muridae; Length Indels Œ AID transgene in Score 594.4; DB 12; Pred. No. 1.3e-149; 0; Mismatches 1; 1. 596
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	420	361 GCTGAGCCCGAGGGCTGCGCGGCTGCACCGCGCGGGGGTGCAATAGCCATCATGACC 420
	360	301 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG 360

Search completed: June 19, 2003, 07:46:31 Job time: 1525.43 secs

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June 18, 2003, 20:16:19; Search time 122.222 Seconds (without alignments) 11000.051 Million cell updates/sec
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1 atggacagcctcttgatgaa......ttcgtactttgggactttga 597
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

; Description	Human activation-i Mouse activation-i Human activation-i Human activation-i Human activation-i Polynucleotide seq Human cDNA encodin Human cDNA encodin
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Score	273.4 273.4 273.4 271 148 118.4 118.4
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cDNA encoding a hu Human RNA metaboli human RNA editing cDNA encoding huma cDNA encoding nove Human prostate can cDNA encoding nove Human polynucleoti Human activation-1 Human activation-1 Human secretory po Gene #3283 used to Human polynucleoti cDNA sequence #359	Human DNA differen Human gene express Genomic sequence # Human cDNA sequenc Human foetal liver Probe #9416 for ge Human brain expres Human bone marrow Probe #8697 for ge Probe #8697 for ge Probe #12563 used Human genome deriv cDNA encoding a no Human APOBEC2 CDNA Human APOBEC2 CDNA Human APOBEC2 GDNA Human immune/haema Human APOBEC2 gene Human secreted pro Human secreted pro Apo-B RNA editing	ALIGNMENTS AAC55312; AAC55312; AAC55312; O5-FEB-2001 (first entry) Human activation-induced cytidine deaminase encoding CDNA SEQ ID NO:7. Activation-induced cytidine deaminase; AID; cytidine deaminase; Immunote control disease; allergy; allergy allergy allergy allergy allergy allergy allergy and the control immune related disease; immunoglobulin A deficiency disease; asthmatic; apphraimological; anti-HIV; dermatological; gene therapy; immunoglobulin A deficiency disease; asthmatigh nephritis; gamma-globulinaemia; atopic dermatitis; allergy; allergy; allergic rolling allergy. Homo sapiens.	induced cytidine deaminase"
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            500 TICAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA 559
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24-JUN-1999;
27-DEC-1999;
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                                                                                                                                                                                                                                                                                                       Claim 3; Page 135-139; 174pp; Japanese.
                                                   99JP-0178999.
28-MAR-2000; 2000WO-JP01918
                                   99JP-0087192
                                                                                                    (NISB ) JAPAN TOBACCO INC.
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597; Conservative
                                                                                                                                                    Honjo T, Muramatsu M;
                                                                                                                                                                                      WPI; 2000-611715/58.
P-PSDB; AAB24198.
                                                                                                                        HONJO
                                                                   27-DEC-1999;
                                 29-MAR-1999;
                                                     24 - JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 597;
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Activation-induced cytidine deaminase; AID; cytidine deaminase; antialergic; antianement antiasthmatic; ophthalmological; anti-HIV; dermatological; antianement; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiantement, antiantement, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
Mouse activation-induced cytidine deaminase encoding cDNA SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "activation-induced cytidine deaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 126-130; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                           BP
                                                                                                     AAC55307 standard; cDNA; 2440
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P-PSDB; AAB24197.
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auto immunodeficiency syndrome; IqG subclass selection disorder; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune related disease; allergy; allergic disease; antiallergic; antianement; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoqlobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; duty allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease;
                                             encoding AID may be used for gene therapy and the antibodies to the AID
          immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
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                                                        protein may be used for diagnosis and treatment of these disorders
 common variable
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                                                                                                      DB 21; Length 2440;
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                                                                              Sequence 2440 BP; 706 A; 546 C; 551 G; 636 T; 1 other;
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87.38; Pred. No. 4 5e-131;
Nicmatches 76;
 DiGeorge disease, ataxia telangiectasia,
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                                                                                                                           Conservative
                                                                                                               Similarity
                                                                                                                 Local Simi
nes 521;
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99.6%; Pred. No. 1e-70;
Live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                        99JP-0178999.
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27-DEC-1999;
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395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429

275 GACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACGCGC

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The present invention describes an activation-induced cytidine deaminase has cytidine activity similar to APOBEC-1. AID has antiallergic. The present cytidine activity similar to APOBEC-1. AID has antiallergic, antianeamic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency colitis, asthma, food allergy, drug allergy, allergic disease, Digeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IT deficiency disease, AIDS (auto immunodeficiency syndrome), elevated contains and lgG subclass selection disconder.
                                                                                                                                                              Activation-induced cytidine deaminase; AID; cytidine deaminase; aminane related disease; allergy; allergic disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; farma qlobulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; atoxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; albs; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                                                                                                                            Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.
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99.6%; Pred. No. 1.3e-70;
u:omatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 163-170; 174pp; Japanese.
              AAC55339 standard; DNA; 11204 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muramatsu M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-611715/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HONJ/) HONJO I.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200058480-A1.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                        05-FEB-2001
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27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000.
                                                      AAC55339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Honjo T,
AAC55339
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immune related disease; allergy; allergic disease; antiallergic; antianament; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; ataxia telangiectasia; common variable immunodeficiency disorder; and najor histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID tolynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease. IgA nephritis, gamma-globulinaemia, atopic dermatitis, altergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rcleic acid encoding activation induced cytidine deaminase, useful target for drug development for immune-related diseases including
                                                                                                                                                                                                                 Human activation-induced cytidine deaminase exon 3 SEQ ID NO:13.
                                                                                                                                                                                                                                                 Activation-induced cytidine deaminase; AID; cytidine deaminase;
8045 CCGGGGTGCAATAGCCATCATGACCTTCAAAGGT 8079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 151; 174pp; Japanese.
                                                                                                      AAC55317 standard; DNA; 271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000WO-JP01918
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24-JUN-1999;
27-DEC-1999;
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DB 21; Length 11204;

Local Similarity 99.6 les 274; Conservative

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Query Match Best Loca Matches

AGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACC 214

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WPI; 2000-611715/58.
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                                                                                                                                                                                                                                                           CATGTGGCCGACTTTCTGCGAGGGACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGC 336
disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder. MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IGE disorder, and IGG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents the exon 3 genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
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                                                                                                                                                                                                                                                                       157 AACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCT
                                                                                                                                                                                                            GGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGGTACGACTGTGCCCGA
                                                                                                                                                                                                                                                                                                        CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCC
                                                                                                                                                                                     AACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCT
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human activation-induced cytidine deaminase exon 2 SEQ ID NO:12.
                                                                                                                                        ;
                                                                                                                 Length 271;
                                                                                                                                        Indels
                                                                                          Sequence 271 BP; 47 A; 95 C; 76 G; 53 T; 0 other;
                                                                                                                                        0
                                                                                                                 Score 271; DB 21;
Pred. No. 1.2e-70;
                                                                                                        45.4%; Scot. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                     GGGGTGCAAATAGCCATCATGACCTTCAAAG 427
                                                                                                                                                                                                                                                                                                                                                                         241 GGGGTGCAAATAGCCATCATGACCTTCAAAG 271
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99JP-0371382
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                                                                                                                                        271; Conservative
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                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200058480-A1
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27-DEC-1999;
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                                                                                                                                                                                                                 (AID). AID structurally relates to an RNA editing enzyme APOBEC and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianeanic, antiasthmatic, ophthalmological, anti-HIV and dermacological activities, and can be used in gene therapy. AID polymucleotides are useful in methods for identifying drugs for the treatment of B cell associated immunos system disorders, immunodeficiency diseases and allergies, such as immunogloulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents the exon 2 genomic DNA sequence of human AID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGG
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Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies –
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                                                                                                                                                                                                 present invention describes an activation-induced cytidine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 148 BP; 35 A; 33 C; 38 G; 42 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No.
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/product= lp547_4
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981..1205
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1165 GTGGGAGGCTGCGGGCCATTCT 1186

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This is the polynucleotide sequence of the clone 1p547_4, which was isolated from a human fetal brain cDNA library using methods which are solated from a human fetal brain cDNA library using methods which are solective for cDNAs encoding secreted protein.

The public sequence of the encoded protein.

The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, hemostatic for manue stimulating (e.g. as vaccines) or suppressing activity, hemostatic cativity, cytokine and cell proliferation/differentiation activity, chemotratic/chemokinetic activity, activity, chemotratic/chemokinetic activity, and tumor activity, receptor/ligand activity, and tumor cativity, receptor/ligand activity, and tumor continuity and solar stated to be useful for generation of bacteria, fundy, viruses and other parasites; effecting continuity continuities activity in the sinclude inhibiting the growth, infection or function of bacteria, fundy, viruses and other parasites; effecting condity characteristics such as, e.g. weight, color, skin, etc. color, skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                Collins-Racie LA,
RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic, diagnostic and research purposes
                                                                                                                                                                                                                                                                        LaVallie ER,
I, Steininger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 104; 125pp; English.
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58.9%;
    99WO-US03458.
                                                                                98US-0075038
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                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
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225; Conservative
                                                                                                                                                                                                                                                                            McCoy JM, La
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-518580/43.
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18-FEB-1999;
                                                                            18-FEB-1998;
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                                                                                                                                                                                                                                                                    Jacobs K,
Treacy M,
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other or cell differentiation activity which is useful for the treatment of cytokines in certain cell populations and may exhibit immune stimulating or immunodeficiencies and disorders e.g. severe combined immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. sultiple actiencis.

Cytokines immune deficiencies and disorders e.g. severe combined immuned for immunodeficiency (SCID), autoimmune disorders actierosis.

Cytokines including are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of print and seases, osteoporosis or osteoartritis, mediated by inflammatory processes, diseases, infammatory processes, diseases, diseases, succeptible and seases, infammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a
                                                                                                                                                                                                                 Human; secreted protein; ss; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans C;
Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCoy JM, Lavallie E, Collins-racie LA,
Agostino MJ, Steininger RJ, Spaulding V,
Fechtel K, Merberg D;
                                                                                                                                                                              Human cDNA encoding a secreted protein lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 580; 619pp; English.
                                              BP.
                                            AAS59293 standard; cDNA; 1534
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04-DEC-2000; 2000US-0729674.
                                                                                                                                16-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639363/73.
P-PSDB; AAU39075.
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Freacy M,
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Clark H,
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RESULT
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(AGOS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune disorder; bacterial infection; fungal infection; cancer; tumour; autofimune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzhelmer's disease; Parkinson's disease; Huntington's disease; activit; hacmophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischemial reperfusion injury; inflammatoryy bowed disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                                                                                                                                                                                                                                                                 457
                                                                                                                           158 ACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG 217
                                                                                                                                                       218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC 277
                                                                                                                                                                                                278 ATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCC 337
                                                                                                                                                                                                            TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGG 397
                                                                                                                                                                   398 GGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                                                                                                                                                                                                        458 AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCT
contraceptive based on the ability of inhibins to decrease fertility female mammals and decrease spermatogenesis in male mammals. The
                                                                                             Gaps
                    proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;
                                                                       DB 22; Length 1534;
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9
                                                                                           0; Mismatches 151; Indels
                                                 Sequence 1534 BP; 495 A; 363 C; 345 G; 331 T; 0 other;
                                                             19.8%; Score 118.4; DB 2.
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                                                                                                                                                                                                                                                                                                                                                                518 CCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA90962 standard; cDNA; 1534
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970S-067454P.
970S-068379P.
980S-070346P.
980S-070643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                Local Similarity 58.9 es 225; Conservative
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially polynucleotides SEO ID NO 1 (ABA90876) and SEO ID NO 1 (ABA90876) and SEO ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 are deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynucleotides and encoded polypeptides have evicatic, anti-inflammatory, immunomodulator, vulnerary, neuroprotective, activin, inhibin, chemotactic, hAemostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, haematopolesis regulators, tissue growth modulators and/or cadherin suppressors. The polypeptides and polynucleotides are useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft versus-host disease; meloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or soteoarthritis; central and peripheral nervous system diseases and neuropathics, central and peripheral nervous system diseases and neuropathics, central and periphers or system diseases and haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 ACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New secreted proteins and encoding polynucleotides, useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steininger RJ, Spaulding V;
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Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Treacy M, Agostine
Clark H, Fechtel K;
                       980S-071304P.
980S-072134P.
980S-073095P.
980S-075038P.
2000US-0539330.
980S-0197886.
98US-070755P
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LAVALLIE E R.
COLLINS-RACIE L A.
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STEININGER R J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLARK H.
                       13-JAN-1998;
22-JAN-1998;
30-JAN-1998;
18-FEB-1998;
30-MAR-2000;
23-NOV-1998;
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Local Similarity
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                                                                                                                                            517
                                                                 TCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCGGCTGCACCGCGCCG 397
                                                                                                                                                                                                                                                                                                                         Human: RNA-associated protein; cell proliferation; cancer; inflammation; immune response; reproductive disorder; actinic keratosis; stateroscierosis; arterioscierosis; beparitis; arterioscierosis; heparitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                              931 AAATGGCTAAATTCATTTCAAAAAAAAAACAAACGTGAGCCTGTGCATCTTCACTGCCGCA 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression of RNA associated proteins -
 GGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                            AAAACCATGAAAGAACTTTCAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCT
                             ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCC
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Azimzai Y, Yue H,
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/*tag a
/product= "RNA-associated protein"
                                                                                                                                                                                                                                                                                                          cDNA encoding a human RNA-associated protein.
                                                                                                                                                                                                      1165 GIGGGAGGCIGCGGCCATICT 1186
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                                                                                                                                                                                   CCAGACAGCTTCGGCGCATCCT 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0158720.
98US-0186815.
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                                                                                                                                                                                                                                                                                            (first entry)
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Hillman JL, Baughn MR,
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22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1998;
                                                                                                                                                                                                                                                                                            25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9;
                                                                                                                                                                                      518
                                                                                                             398
                                                                                                                                                  458
                                                                                                                                                                    1105
                                                                                                                                                                                                                                                                         AAA12409;
                                                                                                                                                                                                                                                                                                                                                                               crauma;
                                    278
                                                                        338
                                                                                                                                                                                                                                    RESULT 10
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Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; parkinson's disease; prion disease; Insomnia; endocrine disorder; AIDES; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; asthma; atherosclerosis; Crohn's disease; rheumatoid arthritis; vaccine; glomerulonephritis; multiple sclerosis; rheumatoid arthritis; vaccine; cancer; cirrhosis; hepatitis; psoriasis; transgentc animal; antiulcer; tranquilliser; drug screening; pancreatitis; renal tubular acidosis; systemic lupus erythematosus; collitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1222 TCTA-----TGATGATCAAGGAAGATGTCAGGAGGGGCTGCGCACCCTGGCCGAGGCTG 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
The present sequence encodes a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, call proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, and disorders which may be treated include actinic keratosis, and disorders which may be treated include actinic keratosis, atteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 GGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1276 GGGCCAAAATTICAATACTGACATACAGTGAATTTAAGCACTGCTGGGACACCTTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 TCTACTICTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 ACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACGGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 1446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    indels
                                                                                                                                                                                                                                                                                                                                     Sequence 1446 BP; 370 A; 374 C; 393 G; 308 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                            Score 116.8; DB 21;
Pred. No. 2.2e-24;
0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human RNA metabolism protein-19 (RMEP-19) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
32..838
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 CCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD24392 standard; cDNA; 1055
                                                                                                                                                                                                                                                                                                                                                                                                        19.6%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.0
Matches 224; Conservative
                                                                                                                                                                                                                                                                                            and cancers, and trauma
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452 744

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The human RNA editing enzyme (REE) is used in a pharmaceutical carrier disorther treatment of cancer, viral diseases and circulatory system disorders. The enzyme issued in vivo for the correct processing of RNA transcripts of genes e.g. change of a codon in apolipoprotein B (apoB) RNA to give a 100 and 48 kDa product transcribed from the same gene. Certain disorders have been linked to incorrect RNA editing, e.g. failure of apo B editing leads to excessive apoB 100 production and hypercholesterolaemia. Other disorders thought to be linked to incorrect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercholesterolaemia. Other disorders unought to the consisting in RNA processing include aberrant alpha-galactosidase processing in RNA processing include aberrant alpha-galactosidase processing in Fabry's disease and neurofibromatosis type I. The enzyme can be produce Fabry's disease and neurofibromatosis type I. The enzyme can be produced in the fabry of the fabry of the fabra of the fabry of the fabry of the fabry of the fabry of the fabra of the fabry of the fabr
                                                                                                                                                             TGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCG
      393 CGCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTT
                                                         685 GGAAGGGGCCTCCGTGAAGATCATGGGCTACAAAGATTTTGTATCTTGTTGGAAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies for immuno-based detection of REE expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 610 BP; 158 A; 154 C; 154 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 114.8; DB 19;
Pred. No. 5.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "RNA editing enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human RNA editing enzyme nucleotide sequence
                                                                                                                                                                                                                                                   539
                                                                                                                                                                                                                                                                                      513 TCTCTCCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV48231 standard; cDNA; 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%;
53.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goli SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-505585/43.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW77092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acquired immune deficiency syndrome, allergies, anaemia, asthma, gout, atherosclerosis, Crohn's disease, diabetes mellitus glomerulonephritis, Hashimoto's thyroditis, multiple sclerosis, osteoarthritis, rheumatoid arthritis, osteoporosis, pancraatitis, systemic lupus erythematosis, ulcerative colitis, and infections); cell proliferative disorders (cancer arteriosclerosis, cirrhosis, hepatitis, psoriasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present sequence is human RMEP-19 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human RNA metabolism proteins (RMEP) and their corresponding cDNA molecules. RMEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementia, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases of the nervous system; inherited, metabolic, endocrine and toxic myopathy; mental disorders (mood, anxiety, schizophrenic disorders) amnesia and Tourste's disorder; autoimmune/inflammatory disorders (AIDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 TAAGAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 TGAGACCCATTGTCATGCAGAAAGGTGCTTCCTCTTGGTTCTGTGACGACATACTGTC 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human RNA metabolism protein for diagnosing or treating nervous system disorders, autoimmune/inflammatory disorders, cell proliferative disorders and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 CCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCGTGGAGCCCCTGCTACGACTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azimzai Y, Au-Young J,
tra S, Policky JJ;
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                                                                                                                                                      /product= "Mature RMEP-19 protein"
/product= "Human RMEP-19 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Batra S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Burford N,
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2000US-202090P.
2000US-210232P.
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225; Conservative
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95..835
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Baughn MR, Yao MG, Bur
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04-MAY-2000;
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                                sig_peptide
                                                                                         mat_peptide
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                                                                                                                                                                                                                                      GAGCCCGAGGGGCTGCGGGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTC 423
                                                                                                                                                                                                                                                       391 TACCAGGAGGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGGACTAT 450
                                                                                                                                                                                                                                                                                            451 GAAGATTTTAAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCT 510
                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                           phorbolin I homologue; cancer; tumour; autoimmune disorder; circulatory system disorder; hypercholesterolaemia; viral infection; neurological disease; neurofibromatosis; transcript editing; detection;
                                                                 CICICITEGITCTEGGACGACATACTGTCTCCTAACAAAGTACCAGGTCACCTGGTAC
                                                                                                                                                                244 ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC
                              GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
                                                                                                           154 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC
                                                                                                                            CTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC
                                                                                                                                                                         CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                             AAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC
                                                                                                                                                                                                                                                                                                              539
                                                                                                                                                                                                                                                                                                                       16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                         --TAAGAACGCTGCCACGTGGAATTGCTCTTC
Gaps
                                                                                                                                                                                                                                                                                                             TGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                editing enzyme; REE-2; human; HEPR homologue; REPR homologue;
15;
232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human RNA editing enzyme REE-2.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            AAA72058 standard; cDNA; 610
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This sequence represents the CDNA encoding human RNA editing enzyme
REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour
CC CDNA library, with the present sequence representing a conseasors. REE-2
has chemical and structural homology with the human apoB mRNA editing
crack schemical and structural homology with the human apoB mRNA editing
crack and a portion of the mRNA editing enzyme photobolin I (43% identity).
CC and a portion of which were defined from tumours, neuronal tissues, immune
CC system cells or synovial tissue from atthritis patients. REE-2 is
therefore thought to be associated with the development of cancer,
CC autoimmune disorders, circulatory system disorders (e.g.
CC hypercholesterolamia), viral infections and neurological diseases (e.g.
CN percholesterolamia), viral infections and neurological diseases (e.g.
C hypertholesterolamia), viral infections and neurological diseases (e.g.
C diagnosis, treatment and prevention of such diseases via the modulation
CC (e.g., an alteration in protein activity). The invention specifically
CC (e.g., an alteration in protein activity). The invention specifically
CC biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGACCTACCTGTGCTACGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
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                                                                                 Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex .
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0; Mismatches 232;
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Local Similarity 53.9%;
hes 289; Conservative (
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17 - NOV - 2000;
    Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligsse; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; inflammatory disorder; anticoagulant; se.
                                                                                         cDNA encoding novel human enzyme polypeptide #636
            AAS41420 standard; cDNA; 950 BP
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2000US - 0.186350.
2000US - 0.186350.
2000US - 0.186374.
2000US - 0.198123.
2000US - 0.2198123.
2000US - 0.2198123.
2000US - 0.2198135.
2000US - 0.2198135.
2000US - 0.219826.
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Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences polypeptides (aAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, including hyperpoliferative disorders (e.g. cancer), carchivascular disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. athma), cardiovascular disorders (e.g. athmanatory disorders (e.g. asthma), cardiovascular disorders (e.g. athmanatory disorders (e.g. infertility) and infectious disorders (e.g. infiluenca). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS1684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention. can also be used in gene therapy. Carguence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
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Pred. No. 7.3e-24;
0; Mismatches 232; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID No 646; 1180pp; English.
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           2000US-0250391
                               2000US-0251030
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05-DEC-2000;
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protein, called prostate cancer antigens, given in ABB56363 to AAB57302. The prostate cancer antigens, given in ABB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antilnfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome polynucleotides may be used for detection of prostate cancer, remosome cidentification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilnfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
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335 ACATCTTGGAGCCCTTGCCCAGACTGTGCAGGGGAGGTGGCCGAGTTCCTGGCCAGGCAC 394
                                                                     364 GAGCCCGAGGGCCTGCGGCGCCTGCACCGCGGGTGCAAATAGCCATCATGACCTTC
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                                        DB 21; Length 987;
                                        Query Match 19.2%; Score 114.8; DB 21; Length Best Local Similarity 53.9%; Pred. No. 7.4e-24; Matches 289; Conservative 0; Mismatches 232; Indels
                    Sequence 987 BP; 231 A; 298 C; 232 G; 224 T; 2 other;
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602638412F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766234 5',
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AJ450317 AJ450317
AJ449745 AJ49745
BB637360 BB637360
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        BF975166 602244657
BF238155 601811880
BG686876 602650861
                                                    BG144705 ut73f07.y
BF975096 602245679
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                  AJ446140 AJ446140
AJ453647 AJ453647
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.g column: 03
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.
Location/Qualifiers
1.743
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                                                                     AJ450296
AJ450317
AJ449745
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BG757089 602715124
                                                                      (without alignments)
12010.756 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                           16154066 seqs, 8097743376 residues
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597
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                                          - nucleic search, using sw model
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE 4766234"

/clone_lib="NIE_MGE 48"

/tissue_type="primary B-cells from tonsils (cell line)"

/lab_host="Dall108 (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;

Site_2: EcoR1; cDNA made by oligo-dT priming.

Directionally cloned into EcoR1XXhol sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using zApp-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL559877 LTI_FL011_BC1 Homo sapiens cDNA clone CSODG003YB14 5 prime , mRNA sequence.
AL559877.1 GI:12905793
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100.0%; Pred. No. 1.3e-168;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                      597; Conservative
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Homo sapiens

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/Jasue_type="B cells from Burkitt lymphoma"
//Issue_type="B cells from Burkitt lymphoma"
//Iab_host="DH10B"
//Iab_host="Ch10B"
//Iab_host="Vector: pCWVSPORT 6; lst strand cDNA was primed with a NotI-coligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCWVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center-Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@ilfetech.com URL: http://fullength.invitrogen.com;
http://fullength.invitrogen.com;
217 c 202 g 226 t 2 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                           : www.genoscope.cns.fr.
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100.0%; Pred. No. 1.4e-168;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                 /organism="Homo saptens"
/db_xref="taxon:9606"
/clone="CSOBG003YB14"
/clone=llb="LTI_FL011_BC1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 597; Conservative
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Indumu.

SM Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SE I (bases I to 953)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt

CONA Library Preparation: Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2108 row: p column: 10

High quality sequence stop: 634.

ES Location/Qualifiers
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/tissue_type="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/lab_host="nbHl0B (phage-resistant)"
/note="organ: lymph, Vector: poTB7; Site_1: XhoI; Site_2:
/note="organ: lymph, Calaptor organ: lymphome of George organ: lymphome organ: lymph
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BQ065440
EQ065440.1 GI:19894486
EST.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhOI;
Site_2: EcoRI: colla made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                           BG758510 872 bp mRNA linear EST 15-MAY-2001 602712721F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853069 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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559 TIGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 615
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLCM1698 row: i column: 06
High quality sequence stop: 836.
Location/Qualifiers
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/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph: Vector: porp3); Site_1: Xho!: Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500pp for average insert size
1:8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
in TR (Life Technologies). Note: this is a NIH_MGC
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602715124F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4855517 5',
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1052)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Au Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.lln.gov
Plate: LLCM2051 row* m column: 14
High quality sequence stop: 665.
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               TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
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Site_2: ECORI; CDNA made by oligo-dT priming.

Site_2: ECORI; CDNA made by oligo-dT priming.

Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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/clone="INAGE:4855517"
/clone="INAGE:4855517"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH108 (phage-resistant)"
                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1704 row: o column: 06
High quality sequence stop: 675.
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          National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 581.8; DB 12
Pred. No. 5.2e-164;
0; Mismatches 2;
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.5%;
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Best Local Similarity 99.5
Matches 594; Conservative
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AUTHORS
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/clone_lib="Wilt_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: BCORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the
following 5' adaptor: GCACGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
57 a 188 c 178 g 170 t
                                                                                                                                                                          693 bp mRNA linear EST 15-MAY-2001
NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851580 5',
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Catarrhini; Hominidae; Homo.
597
                            61 GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGTGAA-GAGGCGTGACAGTGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 693)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapDs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
  541 TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGACTTTGA
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Pred. No. 2e-162;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1694 row: k column: 05
High quality sequence stop: 693.
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4851580"
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Primates;
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Mammalia; Eutheria;
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MRNA sequence.
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Matches 588; Conserva
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BF238155.1 GI:11152074
               99.08;
                             585; Conservative
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BF238155
             Best Local Similarity
Matches 585; Conser
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COMMENT
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BF238155
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/lab.host="DH10B (phage-resistant)"
/lab.host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tobases 1 to 942)

NIH-MGC http://mgc.ncl.nih.gov/.

NIH-MGC http://mgc.ncl.nih.gov/.

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1207 row: a column: 16
High quality sequence stop: 707.

ESS

Location/Qualifiers
359
                                                                      419
                                                                                                                                  BF975166 942 bp mRNA linear EST 22-JAN-2001
602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
                                                          GAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAA
                                                                                                                  GGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGGGGGTGCAAATAGCCATCATGAC
                                                                                                                                                                                                                                  480 AGCCIGGGAAGGGCTGCAIGAAAAITCAGIICGTCTCTCCAGACAGCIICGGCGCAICCI
                                                                                                                                                                                                                                                   Score 560.6;
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/clone="IMAGE:4335639"
/clone_lib="NIH_MGC_48"
                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BF975166
BF975166.1 GI:12342381
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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ORIGIN
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BF975166
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DB 12; Length 942;

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137
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF238155 541 bp mRNA linear EST 14-NOV-20
601811880F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4054915 5',
                                                                                   ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAAGTTCAAAAATGTCCGCTG
                                                                                                                     60 GGCTAAGGGTCGGCGTGAGCCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTAC
                                               1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAA-TTCAAAAATGTCCGCTG
                                                                                                                                                                                                                                                                                          180 CTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTG
                                                                                                                                                                                                                                                                                                                                          GTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 AGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGGGGCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 541)
NHH-MGC http://mgc.nci.nih.gov/.
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-rémail.nih.gov
Tissue Procurement. Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                      Gaps
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM895 row: p column: 20

High quality sequence stop: 541.

1. .541
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 1.4e-157;
thes 4;
Pred. No. 1.46
0; Mismatches
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Similarity
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Matches
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/organism="Homo saplens"
/db xref="taxon:9606"
/clone="IMAGE:4054915"
/clone=lib="WiH_MGC.48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH108 (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xhol sites using the following 5' adaptor: GCACGAGG(6). Size-selected >SODbp for average insert size 18kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using zAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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02650861F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763247 5',
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                 1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
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0
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                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 1.3e-128;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 464; Conserv
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Lissue trocutement: Loudis M. Staduci, M.L., Pril.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Location/Coulifiers

Location/Qualifiers

1. 889

Location/Qualifiers

1. 880

Location/Qualifiers

Location/Qualifiers

1. 880

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG
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Fissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 427.4; DB 12;
Pred. No. 1.8e-117;
0; Mismatches 1;
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GCTAAGGGTCGCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA 120
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Archosauria; Aves; Neognathae; Galliformes; Phaslanidae;
Phasianinae; Gallus.
                   AJ453647
AJ453647 rikenl Gallus gallus cDNA clone 35b23r1, mRNA seguence.
AJ453647
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                                                                                                                                                                    callus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpl.unl-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 68.6%; Score 409.8; DB 9; Best Local Similarity 80.4%; Pred. No. 3.2e-112; Matches 480; Conservative 0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                 /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                          170 t
                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="35b23r1"
/clone_lib="riken1"
                                                                                                                                                                                                                                                           Location/Qualifiers
1. .696
                                                                                                                                                                                                                                                                                                                                                                         173 g
                                                         AJ453647.1 GI:20263743
                                                                                                                                             1 (bases 1 to 696)
Buerstedde, J.M.
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                                                                                              Gallus gallus
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                                                                                  chicken
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                    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 757)
1 (bases 1 to 757)
8 Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology.
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                                                                                                                                                 Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            Length 757;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                           Score 411.4; DB 9;
Pred. No. 1.1e-112;
0; Mismatches 116;
                                                                                                                                                                                                             /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="12j9r1"
/clone_lib="riken!"
/cell_type="bursal lymphocyte"
/dev_strage="2-3 weeks old"
/note="CB inbred strain"
a 205 c 184 g 188 t
                                                                                                                                                                                                                                                                                                                                         68.9%;
80.6%;
                                                                                                                                                                                                                                                                                                                                                                 481; Conservative
                                                                                                                                                                                                    1. .757
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             chicken.
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                                                                                                                                                                                                                                                                                                                                                     Best Local
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          SOURCE
                                                                                   AUTHORS
TITLE
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Gaps

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Length Indels 9

216

276 240 300

360 456 420 516 540

969

541 TIGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTTTGA 597

QΥ

12

RESULT

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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="primary B-cells; from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="organ: B-cells; vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of Galifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                              BF975096 693 bp mRNA linear EST 22-JAN-2001
602245679F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336722 5',
                                          370
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                                                                                                                                                                  284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 693)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Location/Qualifiers
         GCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTT
                         11 GCTGGGGTCCAGATCGGGATCATGACCTTCAAAGACTATTTTTACTGCTGGAATACATTT
                                                                         GTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGT
                                                                                            514 CTCTCCAGACAGCTTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGACTTACGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 CTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 62.5%; Score 373; DB 12; I
al Similarity 100.0%; Pred. No. 3.9e-101;
373; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .693
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:4336722"
                                                                                                                                                                                                                                        574 GCATTTCGTACTTTGGGACTTTGA 597
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                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BF975096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCG 333
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbl.alm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                      522 bp mRNA linear EST 01-FEB-; ut73f07.y1 Soares_mouse_NMGB_bcell Mus musculus cDNA clone IMAGE:3333637 5' similar to TR:Q9WVE0 Q9WVEO ACTIVATION-INDUCED CYTIDINE DEAMINASE.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                        693
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67.0%; Score 400; DB 12; Length 522; 87.1%; Pred. No. 2.5e-109; Live 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAUE.
MGI:1077801
MGI:1077801
Seq primer: -40RP from Glbco
High quality sequence stop: 487.
Location/Qualifiers
c 529
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                              BG144705.1 GI:12648105
                                                                                                                                                                                                                                                                                                     (bases 1 to 522)
                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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nes 439; Conserv
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AJ450296 rikenl Gallus gallus cDNA clone 24m22rl, mRNA sequence.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                     AATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCA
                                                                                   TGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACA
                                                                                                                          1 ATGGACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 366.2; DB 9
Pred. No. 4.5e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
199 c 187 g 170 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Losses 1 to 729)

Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Contact: Buerstedde JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="24m22r1"
/clone_lib="riken1"
                                                                                                                                                                                                                                                                                                    AJ450296.1 GI:20217517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%;
79.8%;
                                                                                                                                                                                                         585 TTTGGGACTTTGA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457; Conservative
                                                                                                                                                                                                                                                                                                                        chicken.
Gallus gallus
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Best Local S:
Matches 457
                                                 121
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AUTHORS
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                                                             TTCCTACGCTACATCTCAGCTTGGGACCTGGACCCAGGCCGCTGCTACCGCATCACATGG
                                                TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCCGACTTTCTGCGAGGG
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earch completed: June 19, 2003, 11:07:28 ob time : 808.004 secs Sequence 5, Appli

Searched:

Run on:

Sequence 30, Sequence 3, Sequence 1,

Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 107, App Sequence 7, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 42, Appli Sequence 43, Appli

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DB 1;
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Pred. No. 1.9e-25;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                US-08-317-880-4

US-08-317-880-4

US-08-396-1

US-08-396-1

US-09-280-116-107

US-09-280-116-107

US-09-280-116-107

US-09-280-116-107

US-09-280-116-107

US-09-527-345-3

US-09-527-345-3

US-09-103-381-14

US-09-103-381-14

US-09-245-281-42

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30
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Sequence 2, Application US/08816241
Sequence 2, Application US/08816241
Sequence 3, Application US/08816241
Sequence 3, Application US/08816241
Sequence 5, Sequence 3, Application US/08816241
Sequence 5, Application US/08816241
Se
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US-08-957-063-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0239 US
TELEPHONE: 415-885-0555
TELEPHONE: 415-885-0555
TELEPHONE: 415-885-0555
TELEPHONE: 415-885-0555
TELEPAX: 415-885-0555
SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Incyte Pharmaceuticals, : 3174 Porter Drive Palo Alto
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Best Local Similarity 53.9
Matches 289; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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; CLONE: 1646833
US-08-816-241-2
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CITY: Pa.
STATE: CA
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7302.178 Million cell updates/sec
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1 atggacagcctcttgatgaa......ttcgtactttgggactttga 597
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                                                                                                                                June 19, 2003, 00:01:09; Search time 25.0728 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seg:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seg:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seg:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-320-878-19
US-08-332-463-14
US-09-015-188-1
US-09-078-294-4
US-09-078-294-4
US-09-078-294-3
US-08-724-974A-1
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US-09-189-060B-73
US-09-105-537-34
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US-09-103-840A-1
US-08-752-760A-1
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US-09-105-537-1
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US-09-718-852-1
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Maximum Match 100%
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Sequence:
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Result Š 3

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Sequence 1, Sequence 1,

US-09-718-815-1

Length 610; Indels

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SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646833
US-09-128-395-2
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Best Local Similarity
Matches 289; Conserv
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                                                                                                                                                                                                                                                                          ACCICCIGGAGCCCCIGCIACGACTGIGCCCGACATGIGGCCGACITICIGCGAGGAAC 303
                                                                                                                                                                       GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTATCCAGGCACATTCTACTTCCAATTTAAAAACCTATGGGAAGCCCAACGATCGGAAC
                                                                                                                                                                                                                                                                                                                                                       CTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC
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                                                                                                                                                                                                                                          TITGGITATCITCGCAA------TAAGAACGCTGCCACGTGGAAITGCICTIC
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APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
STREET: 3174 Porter Drive
COTITY:
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
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APPLICATION NUMBER: 08/816,241
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09128395
Patent No. 6087108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 GAAGATTTTAAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGGCCATTCAAGCCT 510
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                                                                                                                                                                             GAAACTTGGCTGTGCTCTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCTGGAAG
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                                                                                                                                                                                                                                                                                              CTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC
                                                                                                                                                                                                                                                                                                                  244 ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                         76 GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC
                                                                                                                                                                                                                                                       154 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC
                                     Gaps
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Length 610;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
   DB 3;
                   Pred. No. 1.9e-25;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
   Score 114.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
   19.2%;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63.6; DB 2;
Pred. No. 8.2e-10;
                                                                                                                                                                                                                                                                                                                                                 PF-0109 US
                                                                                                             SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-158-682A-3
; Sequence 3, Application US/08158682A
                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/CDCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 891 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 223; Conservative
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
CLONE: 57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                       U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                      94304
                                                                                                                                                                                                                                                               FILING DATE
                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-040-482-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 891;
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Patent No. 5916556
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 63.6; DB 1; 47.0%; Pred. No. 8.2e-10;
                                                                         NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT1
CLONE: 57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.0 Matches 223; Conservative
CURRENT APPLICATION DATA:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                    US-08-687-895-2
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257 CCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGGCGGCTGCACCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTT 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Teng, Bable
APPLICANT: Davidson, Nicholas O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolloprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: ARNOLD, WHITE & DURKEE
321 No. 5550034th Clark Street, Suite 800
                                                                                    Suite 800
                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 56.4; DB 1; 153.4%; Pred. No. 1.3e-07; tive 0; Mismatches 121;
        TITLE OF INVENTION: Composition and Method NUMBER OF SEQUENCES: 18
                           NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 ACTGCTGGAATACTTTTGTAGAAAAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 ACTGCTGGAGGAATTTTGTCAACTAC 517
                                                                                                                                                                                                                                                                                                                                                                                     NAME: COOLLEY, RONAID B.
REGISTRATION NUMBER: 27,187
REERRINGE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEPKX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08015203
Patent No. 5550034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 879 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.4 Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 CCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGT 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5434058
GEMERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street, Suite 800.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08158682A
Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 10.1%; Score 60; DB 1; Length 879; Best Local Similarity 54.1%; Pred. No. 1e-08; Matches 145; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARCD: 085
                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COOLLEY, ROBAIG B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPAN: (312) 744-0090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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23..730
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                          60610
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US-08-158-682A-1
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US-08-158-682A-3
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236 CCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACATTCTGC 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 CGGCTTCCTCGCCGCGCGCGCGCAGCGCTTCAACGAGCTCGACGTCTTCTTCGAGAAGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dalboge, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Rauppinen, Markus
APPLICANT: Rauppinen, Markus
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method of Providing No. 6270968el DNA Sequences
FILE REFERENCE: 4772.204 US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1997-05-12
PRIOR FILING DATE: 1997-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 38; DB 4; Length 1929;
53.3%; Pred. No. 0.072;
tive 0; Mismatches 70; Indels
                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,420C
FILING DATE: 12.No. 6300544-1999
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:

NAME: Medistration NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-21251A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 GCAAGGCTGAGCCCGAGGGGCTGCGGCGGC 385
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73, Application US/09189060B Patent No. 6270968
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1929 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
81..1673
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MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.33
Matches 80; Conservative
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US-09-189-060B-73
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LENGTH: 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 TGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCGAGGGGC 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 IGCGGCGCCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTT 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.4%; Score 56.4; DB 1; Length 8 Best Local Similarity 53.4%; Pred. No. 1.3e-07; Matches 142; Conservative 0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moller, Birger
TITLE OF INVENTION: Cytochrome P450 Monooxygenases
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
CITY: RTP
                                                                                                                                                                               SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 19930209
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                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    CLASSIFCATION. 435
ATTORNEY, AGENT INFORMATION:
NAME: COOlley, Ronald B.
REGISTRATION UNBER: 27,187
REFERENCE/DOCKET NUMBER: 27,187
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 246-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 879 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09380420C Patent No. 6300544 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Halkier, Barbara
Bak, Soren
Kahn, Rachel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
MEDNESS: single
                                                                                           COMPUTER READABLE FORM:
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ZIP: 27709
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                          Illinois
Chicago
                                               USA
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US-09-380-420C-1
                                               COUNTRY:
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                                                                                                                                                                     236 CCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCCTCTACTTCTGTGAGGACC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 CCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCGCGCACCGCGC 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 TGGCCGCTGCTACCGCGTCACCTGGTTCACCTCGTGGAGCCCCTGCTACGACTGTGCCCG
                                                                                                                     176 TGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 GAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCC
                                                    Gaps
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Pred. No. 0.29;
0; Mismatches 129; Indels 0
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Patent No. 6265202

GENERAL INDOMARION:
APPLICANT: Sharman, D.H.
APPLICANT: Liu, H.
APPLICANT: ALO, Y.
APPLICANT: ANG, Y.
APPLICANT: ANG, Y.
APPLICANT: ANG, Y.
CURRENT APPLICATION DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOGTWARRE: FastSEQ for Windows Version 3.0
        Pred. No. 0.058;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAAGGCTGAGCCCGAGGGGC 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRANISM: Streptomyces venezuelae
US-09-105-537-34
    49.38;
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Best Local Similarity 46.9%;
Matches 114; Conservative
Best Local Similarity 49.3
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
3642 CGG 3644
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US-09-105-537-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 GAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCC
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APPLICANT: BETLACH, Melanle C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MODALIE, Robert
APPLICANT: TANG, LI,
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                        APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFWAME: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 129;
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GENERAL INFORMATION:
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Matches 114; Conserv
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APPLICANT: Xue, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36778
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; ORGANISM: Str
US-09-320-878-19
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LENGTH: 2190
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                                                                                  28654 CTGCGACGTCGCCGACCCCCACGCCACCCTCCACGCCATCCCCGCCGCCGAGAC 28713
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                                                                156 GAACGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCC
                                                                                                                                                336 CCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGGCTGCGGCGGCTGCACCGCGC
                                 0; Gaps
6.1%; Score 36.6; DB 3; Length 38506; 46.9%; Pred. No. 0.8;
                                 Indels
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                                0; Mismatches 129;
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)8836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       S-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                              Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; CLONE: pTZgpt-Fls
US-08-232-463-14
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             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 195 CTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAG 254
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Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Kevin J
APPLICANT: Williams, Ira
TITLE OF INVENTION: A Human Gene Encoding Human Chondroitin
TITLE OF INVENTION: 6-Sulfotransferase
FILE REFERENCE: JEFF-0231
CURRENT APPLICATION NUMBER: US/09/015,188C
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
Query Match 6.1%; Score 36.4; DB 1; Length 7 Best Local Similarity 7.0%; Pred. No. 0.42; Matches 19; Conservative 141; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1268 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 TCTGAGGATCTTCACCGCGCGCCTCTACTTCT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-015-188-1
, Sequence 1, Application US/09015188C
; Patent No. 6399358
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 CTTCTGTGAGGACCGCA 358
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 96; Conserva'
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Search completed: June 19, 2003, 11:13:56 Job time : 31.0728 secs

32385,

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Sequence 13, Appl
Sequence 15, Appl
Sequence 5061, Ap
Sequence 5061, Ap
Sequence 4504, Ap
Sequence 4007, Ap
Sequence 4443, Ap
Sequence 4443, Ap
Sequence 4443, Ap
Sequence 2376, Ap
Sequence 25835, Ap
                                                                                                                                               Sequence 25835, App Sequence 2635, App Sequence 763, App Sequence 1, Appli Sequence 1, Appli Sequence 1443, App Sequence 332, App Sequence 332, App Sequence 34, Appl Sequence 34, Appl
US-09-918-995-32385

US-09-966-8803-13

US-09-966-8803-13

US-09-796-692-5061

US-10-040-862-4504

US-10-040-862-4504

US-10-040-862-4607

US-10-040-862-4403

US-10-040-862-4443

US-10-040-862-4443

US-10-040-862-4443

US-09-796-692-4443

US-09-864-761-25835

US-09-864-761-25835

US-09-878-178-1443

US-09-878-178-1443

US-09-878-178-1443

US-09-878-178-1443

US-10-1146-502-1443

US-10-1146-502-1443

US-10-1146-644-332

US-10-1146-644-332
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APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE OF STATE OF OGOOL-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR PLING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                       US-09-988-384B-34
US-09-836-821-34
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09966880A Patent No. US20020164743A1 GENERAL INFORMATION:
                           473
520
520
4689
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4689
4689
  ; NAME/KEY: 3'UTR
; LOCATION: (677)...(2818)
US-09-966-880A-7
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 5'UTR
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LENGTH: 28
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Sequence 13, Appl
Sequence 12, Appl
Sequence 173, App
Sequence 173, App
Sequence 268, App
Sequence 328, App
Sequence 3282, App
Sequence 3282, App
Sequence 30237, Appl
Sequence 30237, Appl
Sequence 9051, Appl
Sequence 9051, Appl
Sequence 9051, Appl
Sequence 9051, Appl
Sequence 5737, Appl
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10937.110 Million cell updates/sec
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                                                                                                                                                             1 atggacagcctcttgatgaa......tcgtactttgggactttga 597
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                                                                                   June 19, 2003, 00:06:39 ; Search time 80.0992 Seconds
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-966-880A-13

US-09-729-674-173

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US-09-729-698-811-268

US-09-966-880A-14
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597
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Listing first 45 summaries
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Scoring table:

Searched:

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Length 2818;

Query Match 100.0%; Score 597; DB 9; I Best Local Similarity 100.0%; Pred. No. 6.1e-189; Matches 597; Conservative 0; Mismatches 0;

1 ATGGACACCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGG

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US-09-864-761-9416 US-09-796-692-5737 US-10-040-862-5737

Score

Result Š. 597 475.4 273.4 273.4 273.4 1118.4 1118.4 1114.8 1114.8 110.4 110.4 78.4 78.4 70.2

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Gaps

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Length Indels 9

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93 ATGGACAGCCTTCTGATGAAGCAAAAGAAGTTTCTTTACCATTTCAAAAATGTCCGTGG 152
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Pred. No. 2.8e-148;
0; Mismatches 76;
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APPLICANT: MUTAMATER, MASAMICH
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: DT/100/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-16-24
PRIOR PLICATION NUMBER: JP 11-178999
PRIOR PLICATION NUMBER: JP 11-178999
PRIOR PLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(2440)
; OTHER INFORMATION: n = A.T.C or
US-09-966-880A-1
                                                                                                       79.68;
87.38;
                                                                                                      Query Match 79.6%
Best Local Similarity 87.3%
Matches 521; Conservative
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                                                    TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC
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GENERAL INFORMATION:
APPLICANT: MUTAMEATSU, MASAMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: 05/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DT. JP00/01918
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-36
NUMBER OF SEQ ID NOS: 36
SCOTWARE: FASLSEQ for Windows Version 4.0
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FEATURE:
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FEATURE:
NAME/KEY: 3'UTR
LOCATION: (690)...(244
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                                                                                        45.4%; Score 271; DB 9; 100.0%; Pred. No. 2.2e-80; Live 0; Mismatches 0;
                                                                      395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429
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APPLICANT: HONJO, Tasuku
APPLICANT: MITAMATUN:
TTLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REPERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PELICATION NUMBER: PCT/JP00/01918
PRIOR PELICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
SPRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFUND OF 33
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APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REPERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
                                                                                                                                                                                          Sequence 13, Application US/09966880A Patent No. US20020164743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 12, Application US/09966880A
; Patent No. US20020164743A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 271; Conservative
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ORGANISM: Homo sapiens
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US-09-966-880A-13
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                                                                                        Length 6564;
                                                                                                                       Indels
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                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429
                                                                                     Score 273.4; DB 9
Pred. No. 2.1e-80;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOUJO, ASSUMICHI
APPLICANT: HOUJO, ASSUMICHI
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
FURENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: DCT/JP00/01918
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: DT 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-03-29
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASSESE for Windows Version 4.0
SEQ ID NO 35
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Patent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
                                                                                     45.88;
                                                                                     Query Match 45.8
Best Local Similarity 99.6
Matches 274; Conservative
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              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 274; Conserv
                                                  US-09-966-880A-10
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LENGTH: 6564
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218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 GAAACTIGGCIGIGCIICACCGIGGAAGGIAIAAAGCGCCGCICAGIIGICICCIGGAAG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 CTCCGCTACATCTCGGACTGGGACCTAGACCTGGCCGCTGCTACCGCGTCACCTGGTTC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCTTCTACTTCTGTGAGGACCGCAAGGCT 363
                                                                                                   ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCC
                                                                                                                                                                             338 TCTACTICTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACGGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 TTTGGTTATCTTCGCAA-----TAAGAACGGCTGCCACGTGGAATTGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 987;
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APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAD.
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN VE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114.8; DB 10;
Pred. No. 8.7e-28;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                             518 CCAGACAGCTTCGGCGCATCCT 539
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Patent No. US20020151681A1
GENERAL INFORMATION:
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Best Local Similarity 53.99
Matches 289; Conservative
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US-09-925-300-699
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US-09-925-300-699
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APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaididing, Vikki
APPLICANT: Fechel, Kinilary
APPLICANT: Pechel, Kinilary
APPLICANT: Genetics Institute, Inc.
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al Similarity 58.9%; Pred. No. 6.9e-29;
225; Conservative 0; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                              Score 148; DB 9; I
Pred. No. 2.3e-39;
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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24.8%; Score 148; DB
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 148; Conservative 0; Mismatches
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CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 173, Application US/09729674 Patent No. US20010039335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-966-880A-12
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; ORGANISM: Homo sapiens
US-09-729-674-173
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                                                                                                                                                                                             LENGTH: 148
                                                                                                                                                                       SEQ ID NO 12
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APPLICANT:
APPLICANT:
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Best Local S
Matches 225
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281 ACGGGCGTCTTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTC 340
                                                                              341 CTCTCTTGGTTCTGCGACGACATACTGTCTCCTAACACAAAGTACCAGGTCACCTGGTAC 400
                                                                                                                                                                                                                                                                              364 GAGCCCGAGGGGCTGCGGGCGCCGCGCGCGGGGTGCAAATAGCCATCATGACCTTC 423
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                                                                                                                     ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC
                                                                                                                                        304 CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                                      424 AAAGATTATTTTACTGCTGGAATACTTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC
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Pred. No. 3.5e-28;
0; Mismatches 1
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APPLICANT: Muramatsu, Masamichi
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-03-29
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Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/09966880A; Patent No. US20020164743A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.1%;
Matches 115; Conservative
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US-09-966-880A-14
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LENGTH: 116
                                       184
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                                                                                                                                    424 AAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCC 483
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                                                           423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
GAGCCCGAGGGGCTGCGCGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTC
                                                                                               489 TACCAGGAGGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGGACTAT
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                                                                                                                                                                           549 GAAGATTTTAAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCT
                                                                                                                                                                                                                    TGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCT 539
                                                                                                                                                                                                                                           15;
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TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 78 dC172

CURRENT APPLICATION NUMBER: US/10/098,841

CURRENT APPLICATION NUMBER: US/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER: OF SEQ ID NOS: 331

SOFTWARE: PLFL-genes Version 1.0

SEQ ID NO 268

LENGT: 1143
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Pred. No. 9.4e-28;
0; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                       Sequence 268, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
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Best Local Similarity 53.9%;
Matches 289; Conservative
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Qian, Xiaohong B.
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Chen, Rui-hong
Wang, Dunrui
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Ma, Yunqing
Wang, Jian-Rui
Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
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Wehrman, Tom
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (128)..(700)
US-10-098-841-268
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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158 ACGGCTGCCACGTGGAATTGCTCTTCCTCGCTACATCTCGGACTGGGACCTAGACCCTG 217
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                                                                                                                                                                                                                                                                                                                                                                                                                   218 GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 ATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCC
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                             0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78.4; DB 9;
Pred. No. 7.6e-16;
0; Mismatches 66;
                                                                                                                                                                                                                                                     Score 104.4; DB 1
Pred. No. 4.1e-24;
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        CURRENT APPLICATION NUMBER: US/09/822,830A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE OF INVESTIGATION CONTROL OF THE REFERENCE: 2041.756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001.07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                       CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
NUMBER OF SEQ ID NOS: 631
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 359
LENGTH: 2151
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58.4%;
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64.1%;
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Best Local Similarity 64.13
Matches 118; Conservative
                                                                                                                                                                                                                                                                                             Matches 223; Conservative
                                                                                                                                                                                            : Homo sapiens
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US-09-918-995-30237
                                                                                                                                                                                                                                                                        Best Local Similarity
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LENGTH: 371
                                                                                                                                                                       TYPE: DNA
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APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Ramalakar
APPLICANT: Glukotck, Kamalakar
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                   APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 3282
LEWGTH: 1348
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Genbank Accession No. US20020142981A1 U03891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110.4; DB 10;
Pred. No. 3.1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(1348)
OTHER INFORMATION: n = a or c or g or t
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APPLICANT: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.5%;
59.3%;
Vockley, Joseph G.
Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wong, Gordon G.
Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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TYPE: DNA
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Matches 15
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                                                                       239 GGTTCACCTCGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAG 298
                    561
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  277
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: MUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
PRIOR PELICATION NUMBER: 60/306,220
PRIOR FLILING DATE: 2001-07-18
PRIOR FLILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOCTWARE: FassESEQ for Windows Version 4.0
GCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 GGTACATATCCTGGAGCCCCTGCACAAGTGTACAAGGGATATGGCCACGTTCCTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

// LCCATION: 1, 2, 3, 1379, 1402, 1403, 1404

// OTHER INFORMATION: n = A/T/C or G

US-10-198-846-13472
                                                                                                                                                                                                                                                                    US-10-198-846-13472
; Sequence 13472, Application US/10198846
; Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9051, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
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Best Local Similarity 55.1°
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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TCTA 354
                                                                                                                                                    TCTA 341
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-796-692-9051
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LENGTH: 1404
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE REFERENCE: 2077.001200
CURRENT PILNG DATE: 2001.03.01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/180,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/220,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/220,903
PRIOR FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR PRILICATION NUMBER: 60/223,378
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Pred. No. 4.4e-13;
0; Mismatches 113;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9051
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US-09-796-692-9051
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Scoring table:

Minimum DB Maximum DB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             imidazoline
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RNA editing
                                                    Description
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SUMMARIES
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AAY95824
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AAE16630
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-Q-/cgn2_1/USP7_L2p.model -DEV-x1p
-Q-/cgn2_1/USP7_L2p.model -DEV-x1p
-Q-/cgn2_1/USP7_L2p.model -DEV-x1p
-Q-/cgn2_1/USP7_L2p.model -DEV-x1p
-DEAA_GENESSEQ_101002 -QFMP-fastan -SUFFIX-n2p.raq -MINMATCH-0.1 -LOOPCL_0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-2D0 -THR_SCORE-PAR_ANS-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-USO9966880_@CGN_1_1_632_@runat_14062003_175523_10297 -NCPU-6 -ICPU-3
-NO_MARP -LAREGOURY -NEG_SCORES-0 -WART -DSPREDCOK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_THREOUT-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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6475.074 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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                GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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(AID). AID structurally relates to an RNA editing enzyme APOBEC.1 and
has cytidine activity similar to APOBEC.1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
colynucleotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunospobulin A (19A) deficiency
disease, 19A nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
disease, Dideorge disease, ataxia telangicetasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
If discorder, and 19G subclass selection disorder. The DNA sequences
encoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for gene therapy and these disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTAAGGGTCGGCGTGAGACCTACCTGTGCTACTAGTGAAGAGGCGTGACAGTGCTACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
auto immunodeficiency syndrome; IgG subclass selection disorder.
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Mismatches:
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Matches:
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99JP-0178999.
99JP-0371382.
                                                                                                      28-MAR-2000; 2000WO-JP01918.
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                                                                                                                                                                                                                           Muramatsu M;
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Best Local Similarity:
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27-DEC-1999;
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TTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activation induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergyc disease; antiallergic; antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atophc dermatitis; allergic collitis; drug allergy; allergic rhinitis; Rosen disease; biGeorge disease; AIDS; ataxia telanglectasia; common variable immunodeficiency disorder;
                                                                                                                                                                                              as
                                                                                                                                    AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
                                                                                                                                                                              TTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAA
                                                                                                                                                                                                                                        GCCTGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
                                                                                                                    GCTGAGCCCGAGGGGCTGCGCGGCTGCACCGCGGGGTGCAAATAGCCATCATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
                                                                                                                                                                                                                                                                                                    594
                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                   TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major histocompatibility class II deficiency disease;
auto immunodeficiency syndrome; IgG subclass selection disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse activation-induced cytidine deaminase SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 131-132; 174pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                       AAB24197 standard; Protein; 198
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99JP-0178999.
99JP-0371382.
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N-PSDB; AAC55307.
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(HONJ/) HONJO
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24-JUN-1999;
27-DEC-1999;
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(first entry)
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Treacy M,
                                                            receptor.
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                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                      GCTAAGGGTCGCCGTGAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACA 120
                                                                                                                                                                                                                                                                                                                                            121 TCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 180
        antianemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (1gA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders.
                                                                                                                                                                                                                                                                                                                                                               09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytidine activity similar to APOBEC-1. AID has antiallergic,
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183
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Mismatches:
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Matches:
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1008.00
95.94%
92.89%
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Best Local Similarity:
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                                                                                                                                               Sequence
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activities which would make them suitable for treating, preventing activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chemotexicic/chemokinetic activity, activin/inhibin activity, chemotexic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, camberal, turnasion suppressor activity, and tumor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting blorhythms or caricadic cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
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human adult blood cDNA
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                                                          secreted protein; cDNA library; clone; transmembrane protein; signal sequence cloning; hybridization cloning; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human secreted proteins used
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RJ;
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Mismatches:
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                                                                                                                                                                                                                                       278..250
/label- Leader/Signal peptide
291..384
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                                                                                                                                                                                                                                                                                                                             291..384
/label= Mature protein
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Agostino MJ, Steininger
Amino acid sequence of 1p547_4.
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GAGACCTACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC 135
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---AspAspGlnGlyArgCysGlnGlvGlyLeuArgThrLeuAlaGluAlaGlyAlaLys 334
                                                                                                                                                                                                                                                                                                                                406 ATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCAT 465
                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; antiinflammatory; immunosuppressive; nortoprotective; antianthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antithermatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immuno deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; parfit-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporcisis osteoarthritis; Alzheimer's disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                        GluThrTyrLeuCysTyrGluValGluArgMetHisAsnAspThrTrpValLeuLeuAsn
                                                     -----TITGGITATCTTCGCAATAAG----------------AACGGCTGC
                                                                       CACGIGGAATIGCICTICCICCGCIACAICTCGGACIGGGACCIAGACCTGGCCGCIGC
                                                                                                                                     HisAlaGluLeuCysPheLeuAspValIleProPheTrpLysLeuAspLeuAspGlnAsp
                                                                                                                                                                                TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGGCCCGACATGTGGCC
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2000US-0729674.
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation of cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of an immunodefication (SCID), autoimmune disorders e.g. severe combined immunodefications (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases of inflammation. The proteins are also useful in the treatment of diseases (GVHD), in the induction of tumour immunity, and disorders including tissue, skin and organ transplantation and in mysloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of cardiac and central nervous system, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, inflammatory processes, disease, Huntington's disease, amylotrophic and central nervous system vessel e.g. stroke, contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
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                                                                                                                                                        Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
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Wong GG;
                    McCoy JM, Lavallie E, Collins-racie LA,
Agostino MJ, Steininger RJ, Spaulding V,
Fechtel K, Merberg D;
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Mismatches:
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                                                           Clark H,
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immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; tumbin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activity haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; infilammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
 297 LysPheIleSerLysAsnLysHisValSerLeuCysIlePheThrAlaArgIleTyr--- 315
                                                                                      |||:::|||||||||:::
335 IleSerIleMetThrTyrSerGluPheLysHisCysTrpAspThrPheValAspHisGln 354
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                       TGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGTGCAA 405
                                     406 ATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCAT 465
                                                                                                                                     GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg 374
                                                                                                                                                                                                                                                                                                                                          Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy;
                                                                                                                                                                                                                                            ABB55784 standard; Protein; 384 AA.
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AGOSTINO M J.
STEININGER R J.
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WONG G G.
CLARK H.
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB55800), especially CABA90980) and encoded proteins (ABB55690), especially CABA90980) and SEQ ID NO 19 (ABA90985) and SEQ ID NO 19 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 closes in number 98599. The polynucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, anti-inflammatory activity and acting as cytokine modulators, and anti-inflammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin and anti-inflammatory activity and acting as cytokine modulators, caheraphes, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial corrections, autoimmune disorders, concer, systemic lupus crythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or costeoarthritis; central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy Drager syndrome; contradiation inflammatory response syndrome, ischaemia-reperfusion or systemic inflammatory response syndrome, ischaemia-reperfusion or systemic inflammatory response syndrome, ischaemia-reperfusion or type-perfusion or stroke; inflammatory bowel disease or consistence or the perpendical performance or systemic inflammatory response syndrome, ischaemia-reperfusion or type-perfusion or stroke; professes or consistence or the perfusion or syndrome.
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                                                                                                                                                      New secreted proteins and encoding polynucleotides, useful in gene
                                                                                                                                                                           therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                      Spaulding V;
    Evans C;
Collins-Racie LA,
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                    Steininger RJ,
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Fechtel K;
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  Jacobs K, McCoy JM,
                      Merberg D, Treacy N
Wong GG, Clark H,
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                                                             immune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                                                                                                                                                                                                        RNA-associated protein; cell proliferation; cancer; inflammation;
ATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCAT
                                                                                 466 GAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
                                                                                                                                                                                                                                                                                                          "potential phosphorylation site"
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349
                                                                                                                                                                                                       Amino acid sequence of a human RNA-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential phosphorylation site"
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/note= "potential glycosylation site"
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                                                                                                                                                           AAY84437 standard; Protein; 384
                                                                                                                CTTCGGCGCATCCTT 540
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375 LeuArgAlalleLeu 379
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167
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Modified-site
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76 GAGACCTACCTGTGCTACTGAAGAGGCGTGACAGTGCTACCATCCTTTTCACTGGAC 135
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                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human RNA-associated protein. The expression of fRNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used immune/inflammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, and atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia and cancers, and trauma.
                                                                                                                                                                                                                                   polypeptides and polynucleotides, useful for preventing and uting a disorder associated with increased or decreased expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TTTGGTTATCTTCGCAATAAG-----------AACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 GlnArgArgGlyPheLeuCysAsnGlnAlaProHisLysHisGlyPheLeuGluGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 HisAlaGluLeuCysPheLeuAspValIleProPheTrpLysLeuAspLeuAspGlnAsp
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316 ---AspaspelnGlyArgCysGlnGluGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAACCAT
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                                                                                                                            35
                                                                                                       Gorgone GA, Pacter
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                         Claim 1; Page 101-102; 131pp; English.
                                                                                                                     Guegler KJ,
98US-0158720.
98US-0186815.
99US-0128660.
                                                                                                                                                                                                                                                                          of RNA associated proteins -
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61.62%
44.32%
35.24%
                                                                          (INCY-) INCYTE PHARM INC
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N-PSDB; AAA12409.
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Best Local Similarity:
                04-NOV-1998;
08-APR-1999;
                                                                                                                                  Hillman JL,
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253 AGCCCCTGCTACGACTGTGCCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC 312
                                                                                                                                                                                                  313 AGTCTGAGGATCTTCACCGCGCGCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG 372
                                                                                                                                                                                                                                                                                         373 GGGCTGCGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT 432
                                                                                                                                                                                                                                                                                                                                                                    154 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 173
                           TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
                                                                            145 CTTCGCAAT------AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
                                                                                                                                 193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG 252
                                                                                             17 PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 36
                                            433 TTTTACTGCTGGAATACTTTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                               CIGCAIGAAAATICAGIICGICICICCAGACAGCIICGGCGCAICCII 540
                                                                                                                                                                                                                                                                                                                                                                                                                      174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11973 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human RNA editing enzyme REE-2.
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                GlyCysProPheGlnProTrpAspGlyLeuGluGluHisSerGlnAlaLeuSerGlyArg 374
 GAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                  Human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
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Conservative:
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Indels:
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|LeuArgGlyIleLeu 379
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                                                   CTTCGGCGCATCCTT
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N-PSDB; AAV48231.
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Best Local Similarity:
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 466
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RNA editing enzyme; REE-2; human; HEPR homologue; REPR homologue; photbolin I homologue; cancer; tumour; autoimmune disorder; circulatory system disorder: hypercholesterolaemia; viral infection; neurological disease; neurofibromatosis; transcript editing; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex
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22-OCT-2001 (first entry)

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This sequence represents the human RNA editing enzyme REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour CDNA library, with the CDNA encoding the present sequence representing a consensus.

REE-2 has chemical and structural homology with the human apoB mRNA celiting protein HEPR (28% identity), the rat HEPR homologue REPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity), and a portion of which were derived from tumours, neuronal tissues, immune system cells or synovial tissue from arthritis patients.

REE-2 is therefore thought to be associated with the devalopment of cancer, autoimmune disorders, circulatory system disorders (e.g., hypercholesterolaemia), viral infections and neurological diseases (e.g., hypercholesterolaemia), viral infections and neurological diseases (e.g., diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein relates to methods of detecting nucleic acids encoding human REE-2 in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
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37 PheThrValGluGlyIleLySArgArgSerValValSerTrpLysThr-----GlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 PheArgAsnGlnValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp
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369.50
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Best Local Similarity:
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AC AAM3
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system such as peripheral nervous system alseases, auch as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic alteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activinhibin activity, chemotactic/chemokinetic activity, heamestatic assays for receptor activity, arthritis and inflammation, leukaemiss and
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                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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                    TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCTTTTCACTGGACTTTGGTTAT 144
PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                CTTCGCAAT------AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC
                                                                                55 PheArgAsnGlnValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp
                                                                                                    ATCTCGGACTGGGACCTAGACCCTGGCCGCTACCGCGTCACCTGGTTCACCTCCTGG
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2000US-0186628.
2000US-0186364.
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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, disquencies or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. cancer), e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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         (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynuclectides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                                                          37 PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys
                                                                                                                                                                                                                                                                                                                                                                                         91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 AGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCTGCGGCGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
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 disorders (e.g. phenylketonuria), inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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                                                                                                                                                                                                   3.86e-33
369.50
58.52%
44.89%
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Query Match:
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 netabolic
                                                                                                                                                           Sequence
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neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                               AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen
 PheArgAsnGlnValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp 105
                                                                                                                                                                                                                                     GlyLeuArgSerLeuSerGlnGluGlyValAlaValGluIleMetAspTyrGluAspPhe 184
                                                                                                                                                                                                                                                                                               185 LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                 AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC
                                                                                                                                                                                                          GGGCTGCGGCGGCGCCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT
                                                                                                                                                                                                                                                                  433 TTTTACTGCTGGAATACTTTTGTAGAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                              193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
                                                                                                                                                  AGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG
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                                                                                                                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                                                                                               Human prostate cancer antigen protein sequence SEQ ID NO:1639
                                                                                                                                                                                                                                                                                                                              CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders such as prostate cancer
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(ROSE/) ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAAW8642-AAA42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to traat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 CTTCGCAAT------AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
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chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
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Zhang J;
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Yang Y,
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Conservative:
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Xu C, Xue AJ,
R, Drmanac RT;
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-065450.
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Wehrman T,
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2000US-0727344
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N-PSDB; AAI59847.
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Wang 2, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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                                                                      WO200153312-A1.
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03-AUG-2000;
14-SEP-2000;
                                                                                                                               26-DEC-2000;
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29-NOV-2000;
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                                            sapiens
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                leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 TITITACIGCIGGAAIACIITIGIAGAAAACCAIGAAAGAACIITCAAAGCCIGGGAAGGG 492
polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
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PheTyrPheGlnPheLysAsnLeuTrpGluAlaAsnAspArgAsnGluThrTrpLeuCys 68
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of aisorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. athritis), neurological disorders (e.g. Alzehmer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. athreosclerosis), conference disorders (e.g. asthma) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                      preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 TTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGACCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG
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                                                                                                       Novel polypeptides and polynucleotides useful for diagnosing,
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79
24
64
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Mismatches:
Indels:
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Matches:
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                               Ruben SM;
(HUMA-) HUMAN GENOME SCI INC.
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369.50
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                              Barash SC,
                                                            WPI; 2001-465566/50.
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                               Rosen CA,
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                             LysTyrCysTrpGluAsnPheValTyrAsnAspAsnGluProPheLysProTrpLysGly 205
                                                                                                                                                                                                                                                                              Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; gene therapy; epllepsy; dementia; stroke; Alzheimer's disease; amnesia; Parkinson's disease; prion disease; insomia; endocrine disorder; AIDS; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; asthma; atherosclerosis; Crohn's disease; rheumatoid arthritis; vaccine; glomerulonephritis; multiple sclerosis; diabetes mellitus; osteoporosis; cancer; cirrhosis; hepatitis; psoriasis; transgenic animal; antiuloer; systemic lupus erythematosus; colitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Invention relates to human RNA metabolism proteins (RMEP) and their corresponding cDNA molecules. RMEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementia, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases; of the nervous system; inherited, metabolic, endocrine and toxic myopathy; mental disorders (mood, anxiety, schizophrenic disorders) amnesia and Tourette's disorder; autoimmune/inflammatcry disorders (AIDS-acquired immune deficiency syndrome, allergies, anaemia, asthma, gout,
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|LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 221
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tra S, Policky JJ;
                                                             CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22..268
/label= Mature_RMEP_19_protein
                                                                                                                                                                                                                                                  Human RNA metabolism protein-19 (RMEP-19).
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N, Batra S,
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Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid arthritis, osteoporosis, multiple sclerosis, osteoarthritis, rheumatoid ulcerative colitis, and infections; cell proliferative disorders (cancer attribosclerosis, pencientis, psorlasis); cell proliferative disorders (cancer attribosclerosis, cirrhosis, hepatitis, psorlasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present sequence is human RMEP-19 protein.
                                                                                                                                                                                                                                                                                                                                                                           95 PheTyrPheHisPheLysAsnLeuLeuLysAlaCysGlyArgAsnGluSerTrpLeuCys 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 CysTrpLysAsnPheValTyrSerAspAspGluProPheLysProTrpLysGlyLeuGln 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; infectious disorder; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                          91 TACGTAGTGAAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                         PheThrMetGluValThrLysH1sH1sSerAlaValPheArgLysLysGlyValPheArg
                                                                                                                                                                                                                                                                                                                                              199 GACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGGCCCGAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ThrilePheThrAlaArgLeuCysTyrPheTrpAspThrAspTyrGln---GluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 CGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 CysSerLeuSerGlnGluGlyAlaSerValLysIleMetGlyTyrLysAspPheValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 GAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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71
27
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                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                          2.43e-29
336.50
56.32$
40.80$
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                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                  268
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2000US - 0237039
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26. SEP-2000;
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29. SEP-2000;
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20. CGT-2000;
20
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18-APR-2000;

77-JUN-2000;

30-JUN-2000;

30-JUL-2000;

11-JUL-2000;

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14-AUG-2000;

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06.SEP-2000;
08.SEP-2000;
08.SEP-2000;
08.SEP-2000;
08.SEP-2000;
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08.SEP-2000;
08.SEP-2000;
08.SEP-2000;
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01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
             Homo sapiens.
                                                                                     17-JAN-2001;
                                                            02-AUG-2001
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TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTCACTGGACTTTGGTTAT 144 87 PheArgAsnGinValAspSerGluThrHisCysHisAlaGluArgCysPheLeuSerTrp 106 GGGCTGCGGCGCCTGCACCGCCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTAT 432 CTTCGCAAT------AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192 AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC AGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG 193 ATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGG 272 75 25 67 14 US-09-966-880A-7_COPY_80_676 (1-597) x AAU23799 (1-272) Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.39e-28 323.50 55.25% 41.44% 29.38% Percent Similarity: Best Local Similarity: Alignment Scores: 49 45 107 253 127 313 147 373 166 Query Match: DB: ò q ò g Q õ ò g à 9 ò g

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        Db
        186 LysTyrCysTrpGluAsnPheValTyrAsnAsp-AsnGlu-------ProAlaProLy 202

        Qy
        493 CTGCATGAAAATTCAGTTCGTC---TCTCCAGACACACTTGGCGCATCTTTTGCCCTG 549

        Db
        202 sCysLeuSerLeuValLeuThrArgGlyCysSerSerGlnAlaAlaGlyTrpLeuProCy 222

        Qy
        550 T 550

        Db
        222 s 222

        Db
        222 s 222

        Search completed: June 14, 2003, 18:25:30

        Job time: 28:5713 secs
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hypotherical prote alkaline nuclease hypotherical prote DNA-binding protei malate synthase -nuclear pore glyco exo-alpha-sialidas

nucleoporin p62

glycoprotein precu hypothetical prote CED-6 protein - Ca

achaete-scute homo hypothetical prote

conserved hypothet

T02345 S41819 JC5169 JC5169 JC5169 SAD293 SAD293 SAD293 C25339 VGBEKG T16484 T16484 T16484 T16494 T151382 T151

phosphogluconate d phenylalanine-tRNA atrophin-1 - human atrophin-1 - human Balbiani ring 2 ch probable acid-CA unknown protein, 4

fucosyltransferase hypothetical prote probable phosphate

F36791 G72754 G72754 C64601 E70546 AD0345 S65762

chitinase (EC 3.2. hypothetical prote

ALIGNMENTS

hypothetical prote immediate-early pr

- human

mucin 5AC

A69831 A96717

probable phospĥoen

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RESULT 1

G01233
phorbolin I - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence_rev
C; Accession: G01233
R; Madsen, P.P.
submitted to the EMBL Data Libran
A; Reference number: G06330
A; Accession: G01233
A; Status: preliminary; translated
A; Molecule type: mRNA
A; Residues: 1-116 < MAD>
A; Residues: 1-116 < MAD>
A; Cross-references: EMBL:003891;
C; Superfamily: apolipoprotein B r
VBBBGGGL/
                                                                                                                                                                                                                    80.5
80.5
80.5
80
80
80
80
79.5
Command line parameters:
-MODEL-frame+_n7P.model -DEV=x1p
-MODEL-frame+_n7P.model -DEV=x1p
-MODEL-frame+_n7P.model -DEV=x1p
-Q-Cgn2_1/USPTQ_spool/US09966880/runat_14062003_175525_10329/app_query.fasta_1.9493
-Q-Cgn2_1/USPTQ_spool/US09966880_runat_10P.rpr -MINMATCH=0.1 -LOOPCL=0 -LCOPEXY=0
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 -cdi -LIST=45
-OOTINGN=200 -THE_SCORE=pct -THR_MAX=100 -TALIGN=100 -LOOPC-10-10
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-DEV_INBOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -SGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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6680.033 Million cell updates/sec
                                                                 June 14, 2003, 18:12:33; Search time 17.1832 Seconds
                                                                                                        US-09-966-880A-7_COPY_80_676
1101
1 atggacagcctcttgatgaa......ttcgtactttgggactttga
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                               - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                           283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                                                                                                            BLOSUM62
Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phorbolin I - huma	apolipoprotein B m	homeotic protein a	hypothetical prote	cyclin-dependent k	virion protein hom	interferon respons	hypothetical prote	extensin homolog F	GAP-associated pro				
SUMMARIES	ID	G01233	A53853	159323	JC4269	148249	159577	S58850	S63464	JC7317	JC1306	A46241	T13412	T04859	A38218
	DB	7	7	7	~	7	7	7	~	~	~	7	7	7	~
	Query Match Length DB	116	236	236	229	229	229	295	369	568	504	277	2342	839	1493
æ	Query Match	22.3	20.4	19.7	19.2	19.2	18.0	9.4	8.9	8.6	9.1	8.4	8.4	8.3	8.0
	Score	245	225	216.5	211	211	198	97.5	97.5	94.5	94	93	92.5	91.5	88.5
	Result No.		7	m	4	Ŋ	9	c 2	80	6	c 10	11	12	13	14

C:Species: Homo sapiens (man) C:Species: Homo sapiens (man) C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-Apr-2002 C:Date: 21-Dec-1996 #sequence_revision 061233 R:Madsen, P.P. submitted to the EMBL Data Library, December 1993 A;Reference number: G06330 A;Reference number: G06333 A;Recession: G01233 A;Recession: G012333 A;Recession: G012333 A;Recession: G012333 A;Recession: G012333 A;Recession: G012333 A;Re	116 51 51 32 32 10 3	226 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACAT 279	280 GTGGCCGACTTTCTGCGGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGGCGCCTC 339	340 TACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGCTGCGGGGGGCTGCAC 390
C.Species: Homo saptens (man) C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997; C.Accession: 601233 C.Macsen, P.P. Submitted to the EMBL Data Library, December 1993 A.Reference number: G06330 A.Reference number: G10833 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-116 MADECULE Type: MRNA A.Residues: 1-116 MADECULE Type: MRNA A.Cross-references: EMBL:003891; NID:9436940; PIDN: C.Suberfamily: apooliboprotein B mRNA editing enzyme	Alignment Scores: 2.31e-15 Length: Score: 245.00 Matches: Percent Similarity: 61.82% Conservative: Best Local Similarity: 46.36% Mismatches: Query Match: 22.25% Indels: DB: 20.25% Gaps: US-09-966-880A-7_COPY_80_676 (1-597) x G01233 (1-116)	TCCTGGAGCCCCTGCT 	AACCCCAACCTCAGTC:	GCTGAGCCC ::: TyrAspProLeuTyrL
C:Species: Homo sapiens (man) C:Date: 21-Dec-1996 #sequence_revision 06-Jun-199 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-199 C:Accession: 061233 A:Reference number: G06330 A;Reference number: G06330 A;Residues: 1-116 <	2.31e-15 245.00 61.828 .y: 46.368 .y: 42.258)GTCACCTGGTTCACC 	GACTTTCTGCGAGGG 	TGTGAGGACCGCAAG
C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 21-Dec-1996 #sequence C.Accession: G01233 submitted to the EMBL Data Li A.Reference number: G0530 A.Accession: G01233 A.Status: preinminary; transl A.Molecule type: mRNA A.Residues: 1-116 < MAD> A.Cross-references: EMBL:U038 A.Cross-references: EMBL:U038	Alignment Scores: Pred. No.: Score: Percent Similarity: Query Match: DB: US-09-966-880A-7_COPY_	226 TACCGC 7 TYFATG	280 GTGGCC 27 ValArg	340 TACTTC 47 Tyr
C; Don Submac A; Rem A; Rem A; Rem A; Rem C; Sul	Alignm Pred. Score: Percen Best L Query DB:	Qy Db	Qy Db	Qy Db

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C;Accession: IS9323; S45253
R;Lau, P.P.; Zhu, H.J.; Baldini, A.; Charnsangavej, C.; Chan, L.
Proc. Natl. Acad. Sci. U.S.A. 91, 8522-8526, 1994
A;Title: Dimeric structure of a human apolipoprotein B mRNA editing protein and cloni
A;Reference number: IS9323; MUID:94359963; PMID:8078915
                                                                                                                                A; Accession: I59323
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-236 <RES>
A; Cross-references: GB:126234; NID:9609447; PIDN:AAA64230.1; PID:9604539
A; Cross-references: GB:126234; NID:9609447; PIDN:AAA64230.1; PID:9604539
B; Hadjiagapiou, C.; Glannoni, F.; Funahashi, T.; Skarosi, S.F.; Davidson, N.O.
Nucleic Acids Res. 22, 1874-1879, 1994
A; Title: Molecular cloning of a human small intestinal apolipoprotein B mRNA editing
A; Reference number: S45253; MUID:94268910; PMID:8208612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AATAAGAACGCTGC---CACGTGGAATTGCTCTTCCTC---CGCTACATCTCG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - mouse C;Species: Mus musculus (house mouse)
C;Species: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
            C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 ArglysGluAlaCysLeuLeuTyrGluIleLysTrpGlyMetSerArgLysIleTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 SerSerGlyLysAsnThrThrAsnHisValGluValAsnPheIleLysLysPheThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: RNA editing; edits codon CAA to UAA in apolipoprotein C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain C;Keywords: dimer; hydrolase; intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC--
                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA A; Residues: 1-52, TT, 54-82, TT, 84-236 <HAD> A; Residues: 1-52, TT, 54-82, TT, 84-236 <HAD> C; Comment: This enzyme is a cytidine deaminase. C; Comment: This protein is found only in the small intestine. C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
44
31
42
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:371870; OMIM:600130
A;Map position: 12p13.1-12p13.1
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTGGAATACTTTTGTA 456
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59.52%
34.92%
19.66%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: APOBEC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                                                                                                                                                                    apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - rabbit C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 07-0c1-1994 #sequence_revision 07-oct-1994 #text_change 18-Aug-2000
C; Accession: A53883
R; Yamanaka, S.; Poksay, K.S.; Balestra, M.E.; Zeng, G.O.; Innerarity, T.L.
J; Biol. Chem. 269, 21725-21734, 1994
A; Title: Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc motif ributed.
          450
                                                                                                       70 CGGCGTGAGACCTACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACATCCTTTTCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTC 243
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|ProGlyValThrLeuIleIlePheValAlaArgLeuPheGlnHisMetAspArgArg--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCCCGAGGGGTGCGGCGGCGCGCGGGGTGCAAATAGCCATCATGACCTTC 423
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TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ArgLysGluAlaCysLeuLeuTyrGluIleLysTrpGlyAlaSerSerLysThrTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 CTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGC---CACGTGGAATTGCTCTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A Reference number: A53853; MUID:94342367; PMID:8063816
A Accession: A53853
A Status: pre-iminary
A Molecule type: mRNA
A Residues: 1-236 < YAM>
A Residues: 1-236 < YAM>
A Residues: 1-236 < YAM>
C Soss-references: GB:U10695; NID:9506180; PIDN:AAA56718.1; PID:9506181
C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C; Keywords: hydrolase; zinc
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26
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                  511 CGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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Gaps:
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Pred. No.:
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C; Keywords: hydrolase
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C; Species: Mus musculus (house mouse)
C; Date: 0.2-uul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
C; Accession: 148249; 149289; 149286; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 149288; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 14928; 
Richard M.; Jazaki, Y.; Harada, K.; Yagyu, H.; Shimada, M.; Yazaki, Y.; Yamada, N.; Blochem. Biophys. Res. Commun. 214, 653-662, 1995
A;Title: Cloning and structural analysis of the mouse apolipoprotein B mRNA editing FA; Reference number: JC4269; MUID:95408299; PMID:7677778
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
C;Comment: This protein belongs to the cytidine deaminase gene family.
C;Comment: This protein B mRNA editing enzyme, catalytic chain 1
C;Keywords: hydrolase; zlnc finger
F;48-96/Region: zinc finger HHCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AsnArgGlnGlyLeuArgAspLeuIleSerSerGlyValThrIleGlnIleMetThr 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 CTC---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG 240
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A;Accession: I49286
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Matches:
Conservative:
Mismatches:
Indels:
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A;Accession: 149287
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-229 <RE2>
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apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: 159577
R;Teng, B.; Burant, C.F.; Davidson, N.O.
Science 260, 1816-1819, 1993
A;Telle: Molecular cloning of an apolipoprotein B messenger RNA editing protein. A;Reference number: 159577; MUID:93289362; PMID:8511591
A;Accession: 159577
A;Accession: 159577
A;Residue; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-299 cRES
A;Cross references: GB:L07114; NID:9467808; PIDN:AAA17394.1; PID:9347165
C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-229 <RE3>
A;Cross-references: EMBL:U2262; NID:g899504; PIDN:AAC52212.1; PID:g899505
A;Accession: 14928
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-229 <RE4>
A;Cross-references: EMBL:U22264; NID:g899508; PIDN:AAC52214.1; PID:g899509
C;Genetics: AGI:103298
A;Cross-references: MGI:103298
A;Cross-references: MGI:103298
A;Cross-references: MGI:103298
A;Introns: 6/1; 15/2; 148/1; 187/3
C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C;Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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424
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Mismatches:
Indels:
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Matches:
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55.30%
37.12%
19.16%
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Best Local Similarity:
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Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	7.82e-11 198.00 47.06% 32.94% 17.98%	Length: Matches: Conservative: Mismatches: Indels:	22 24 24 8 28 24		Align Pred. Score Percer
60-SN	-966-880A-7_COPY_8	_80_676 (1-597) x)		Best Query
Qy	70 CGGCGTGAG	TACCTGTGC	GTAGTGAAG		G 105	. DD:
QQ	33 ArgLysGluThr		::: GluIleAsnTrpGly			20 0
Qy	106 CGTGACAGT	GCTACATCCTTTTCA	CTGGACTTTGGTTAT	106 CGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTTCC		3 2
qq	 53 HisThrSer	 HisThrSerGlnAsnThr	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AsaLvs	9	S :
Qy	166 CACGTGGAA	TTGCTCTTCCTC	CGCTACATCTCGGAC	TGGGACCTAGACCCTGGCCGC		<u> </u>
qa	61 HisValGluv	::: (:::::: LysPheThrThrGlu			3 8
ογ	223 TGCTACCGC	GTCACCTGGTTCACC	TCCTGGAGCCCCTGC	PACGACTGTGCCCGACATGTC		Z 2
qa	81 ArgCysSer]	:::		ArgCysSerIl@ThrTrpPheLeuSerTrpSerProCysGlyGluCysSerArgAlalle		2 0
٥y	283 GCCGACTTTCTG	CTGCGAGGGAACCCC	AACCTCAGTCTGAGG	GCCGACITICIGCGAGGGAACCCCAACCICAGICIGAGGAICTICACCGGCGCGCTCTAC	342	. q
qa	101 ThrGluPhel	LeuSerArgTyrProl	HisValThrLeuPhel	ThrGluPheLeuSerArgTyrProHisValThrLeuPhelleTyrIleAlaArgLeuTyr	120	δò
ΟŊ	343 TTCTGTGAGG	GACCGCAAGGCTGAGG	CCGAGGGGCTGCGG	TTCTGTGAGGACCCCAAGGCTGAGGCGCTGCGGCGGCTGCACCGCGGGGTG	5 402	· qa
qq	121 HisHisAla	AspProArgAsn	ArgGlnGlyLeuArgA	HisHisAlaAspProArgAsnArgGlnGlyLeuArgAspLeuIleSerSerGlyVal	139	^O
οy	403 CAAATAGCCA	ATCATGACCTTCAAAC	SATTATTTTACTGCT	CAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTAGAAAAC	: 462	7 원
qq	140 ThrileGlni	IleMetThrGluGlnC	3luSerGlyTyrCysT	ThrileGlnileMetThrGluGlnGluSerGlyTyrCysTrpArgAsnPheValAsnTyr	159	ΛŌ
οy	463 CATGAAAGAA	ACTTTCAAAGCCTGG	SAAGGGCTGCATGAAA	CATGAAAGAACTTTCAAAAGCCTGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGA	522	. 4 <u>0</u>
Ob	160 SerProSerA	 AsnGluAlaHisTrp		euTrpValArgLeu	177	, vo
Οy	523 CAGCITCGGC	CAGCTTCGGCGCATCCTTTTGCCCCTGTAT	TGTAT 552			ī 2
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C;Specie C;Date:	38: Junonia coeni 19-Mar-1997 #seq	.a Nence revision	19-Wart1007 ##0	7 7		qq
C; Access	sion: S58850; S58	1851	133/ # FE	*rext_cnange 1/-Nov-2000	0	e mode
Nature 3	1, K.W.; Nagy, L. 372, 458-461, 199	; Selegue, J.;	Gates, J.; Carro	oll, s.		S63464
A; Title: A; Refere	Evolution of hor	meotic gene reg	ulation and fund 56; PMID:784082;	es and	butterflies.	Nypothe NyAlter
A; Access A; Status	ton: SS8850 : nucleic acid se	equence not sho	wn; translation	not shown		C; Speci C; Date:
A; Residu	te cype: mknA es: 1-295 <war></war>					C; Acces R; Wang,
A;Cross- A;Note:	references: EMBL the nucleotide se	:L41931; NID:g7 equence was sub	97276; PIDN:AAA6 mitted to the EN	58460.1; PID:9797277 (BL Data Library May	000	submitt A;Refer
A; Access A; Status	ion: S58851 : nucleic acid se	equence not show	wn: translation	3	133	A; Acces A; Molec
A;Molecu A;Residu	le type: mRNA es: 214-271 <wa2></wa2>	. ^		310.811		A;Resid A;Cross
A; Cross- A; Note:	references: EMBL: the nucleotide se	:L42135; NID:98	33750; PIDN:AAA6	8461.1; PID:9833751 Br. Data Library	900	C;Genet A;Gene:
C;Geneti A;Gene:	cs: abd-a			de 'frage san	100	A; Wap p
C; Superr C; Keywor	C:Superfamily: unassigned homeobox proteins; homeobox homology C:Keywords: DNA binding; homeobox; nucleus; transcription regulation F:315-3717 homein; homeobox;	d homeobox prote homeobox; nucle	eins; homeobox h eus; transcripti	homeobox homology transcription regulation		Alignme
. 14-614	1/Volnain: nomeodo	ox homology <ho)< td=""><td>△</td><td>1</td><td></td><td>Score. N</td></ho)<>	△	1		Score. N

Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	0.363 97.50 32.818 21.88 9.43%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	295 42 21 58 58 7	
 3-996-60-SN	-880A-7_COPY_8	80_676 (1-597) x	S58850 (1-295)		
 Qy do	462 GTTTTCTACA 25 ValHisTyrC	AAAAGTATTCCAGCA(::::: 31yAlaValProGln(GTAAAAATAATCTTTG 3lnGlyHisGluMetG	GTTTTCTACAAAAGTATTCCAGCAGTAAAATAATCTTTGAAGGTCATGATGGCTATTTG 	403
 Oy Db	402 CAC		099000	CCCGGCGCGGTGCAGCCGCCGCAG	376
	. L	CTCAGCCTTGCGGTCC	TTCACAGAAGTAGAGG	TOTAL CONTROLL OF THE CONTROLL	64 316
 qa	 65 ProProTyrA	 AspArgLeuGlyTyr1	:::::!!! [yrGlnGlnMetGluG	 	84
Qy 3 Db	315 ACTGAGGTTG ::: 85 Ser	3GGGTTCCCTCGCAGA 	ACTGAGGTTGGGGTTCCCTCGCAGAAAGTCGGCCACATGTCGGGC:::	TCCCTCGCAGAAAGTCGGCCACATGTCGGGC	271
 0γ 2	270			ACAGTC	265
 Db 1	100 GlyProAsnG	lyHisGlnProProT	hrProAlaValTyrT	GlyProAsnGlyHisGlnProProThrProAlaValTyrThrSerCysLysLeuGlnAla	119
Oy 2 Db 1	264 GTAGCAGGGG 120 AlaAlaGlyT	GTAGCAGGGGTCCAGGAGGTGAACCAGGTGACGC AlaAlaGlyThrAlaGlyGlyValProGlySer	CAGGTGACGCGGTAGC roGlySer		205
 0y 2	204 CCAGTCCGAG	ATGTAGCGGAGGAAG	AGCAATTCCACGTGGC	CCAGTCCGAGATGTAGCGGAAGAGAAATTCCACGTGGCAGCCGTTCTTATTGCGAAG	145
 Db 1	131 ProProLeuG	 ProProLeuGluGlnAlaGlnGlnMetProHisHis	 etProHisHis		142
Oy 1	144 ATAACCAAAG	TCCAGTGAAAAGGAT	GTAGCACTGTCACGCC	ATAACCAAAGGTCAGTGAAAAGGATGTAGCACTGTCAGCTCTTCACGTACGT	85
			methispr		151
 Oy Db 11	52	CGCCGroproHisGlnH:	ACCCTTAGCCCAGC ::: isLeuMetT.yrProVa	GTAGGTCTCACGCCGACCCTTAGCCCAGCGGACATTTTGAATTGGTA	37 171
Oy 3	9 0	AAGAAACTTCCTCCGGTTCATCAAGAGGCTGTCCAT :::::: ::: ThrdlnMetProProMetHisGlnGlnSerMetHis	AGGCTGTCCAT 1::::::: 		
 RESULT 8 S63464 Nypothetical NyAlternate C; Species: S C; Accession: R; Wang, Y:; Submitted to A; Reference A; Accession: A; Mang, Y:; A; Mang, M	cal protein YPLC e names: hypoth : Saccharomyces > May-1996 #sequent > Ahmed, A.; Bu to the EMBL Dat to the EMBL S63464 i. 1-369 (WAN) :: 1-369 (WAN)	018w - yeast (Schettcal protein cerevisiae Lence_revision lassey, H.; Fortisa Library, Septisa Library, Sept	_ # Ø 5	cerevisiae) text_change 06-Feb-1998 en, J.D.; Hall, J.; Storms, 1039459; MIPS:YPL018w	ms, R.K.;
 COL	, 6	U. 300 97.50 M	Lengin: 369 Matches: 50	თ _	

Percent Simi Best Local S Query Match: DB:	Percent Similarity: 37.33% Conservative: 34 Best Local Similarity: 22.22% Mismatches: 70 Query Match: 2 Indels: 71 DB: 2 Gaps: 11	Length:
-996-60-SN	-880A-7_COPY_80_676 (1-597) x S63464 (1-369)	94.50 Matches: 35.96% Conservative:
cy gp	4 GACAGCCTCTTGATGAACCGGAGGAAGTTTCTTACCAATTCAAAATGTCCGCTGGGCT 63 ::	Hest Local Simitarity: 25.37% Mismatches: 49 Query Match: 8.58% Indels: 65 DB: 8
ζ, Db	64 AAGGGTCGGCGTGACCTACCTGCTACGTAAGAGGCGTGACAGTGCTACATCC 123 76GlothitycGloasoileleumetivsGluasoasorivstr 90	US-09-966-880A-7_COPY_80_676 (1-597) x JC7317 (1-568) QY
Qy	GACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC	4 AlaThrAlaThrAlaGlyThrAlaAlaCysSerSerSerSerSerSerArgGlyGlySer 23
qa	91AsplieLeuGln 97	Qy 209 TAGACCCIGGCCGCTGCTACCGCGTCACCTGGTTCACCTCGTGGGGCCCTGCTACGACT 268
oy Dp	181	269 GTGCCCGAC
oy (Db 43 ProProGluProLeuArgLysProArgMetAspProArgArgGlnAlaAlaLeuSer 62 Qy 278ATGTGGCCGACT 289
g ò	ilb AlalieserAsparglysArgValGiuArglieAsnGlyLeuThrAsnLeuGInLysGlu 137 256CCCTGCTACGACTGTGCCCGACATGTGGCGACTTTCTGCGAGGGAACCCCAAC 309	 Db 63 PheLeuThrAsnIleSerLeuAspGlyArgProProLeuGlnAspHisGluTrpGlyGly 82
Dp		290 TTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACGGGGGCCCTTACTTCTGTG
٥y	310 CTCAGTCTGAGGATCTTCACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC 369	DD 83 GLYGLUGLUGLYGLY GLYTHTLYSPTGGLYALA 93 OV 350 AGGACGGAAGGCTGAGCCGGAGGGGCTGCGGGGGTGCACCGGGGGGGC
qa	Σ	94ArgAlaArqLeuSerLeuLeuAlaAlaGlyCysAsnAlaPheSerAlaProGly
oy G	370 GAGGGGCTGCGCGCCGCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGAT 429 ::: ::: 170 GlnSerArgAspArgValHisAsnAspGlyIleGluValLeuValValAsnTyrLys 188	404 AAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGA
٥y	TGG,	112ThrAlaAlaAlaProTrpThrAlaGlySerGlySerProCys 12
QQ	:::	Oy 446ATACTTTTGTAGAAAACATGTAGAAAAAGCCTGGAAGGGC 493 127 ProLeuProProSerLeuValProArqualLeuGlyGluProSerGlnProProArqser 146
oy e	460 AACCATGAAAGAACTTTCAAAGCCTGGGAAGGCTGCATGAAAATTCAGTTCTC 516 3.:	494 TGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCACATCC 538
ò	TOTAL THE TABLE TO THE TABLE TH	Db 147 AlaProAlaValThrGlyAlaGlnLeuGlnLeuProAspGlyProGlyGlyAla 164
G Q		RESULT 10 JC1306
δλ	556 GITGATGACITACGA 570	VILION procein nomolog - bovine nerpesvirus i N:Alternate names: alpha TIF: BHV-1 protein homolog; ICP25; Vmw65; VP16 C;Species: bovine herpesvirus 1
DD RESULT 9	247 PheAspLysIleLys 251	C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 20-Jun-2000 C;Accession: 071306; 52429 B:Carnenter D F: Misra V
Cyclin-dep Cyclin-dep C; Species: C; Date: 08	JC7317 cyclin-dependent kinase 3 interactor-1 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 08-Sep-2000	A;Title: Sequences of the bovine herpesvirus 1 homologue of herpes simplex virus typ A;Reference number: JC1306; MUD:93012995; PMID:1327963 A;Accession: JC1306 A;Accession: JC1306 A;Molecule type: DMA
R; Matsuoka Blochem. E A; Title: N	a, M.; Matsuura, Y.; Semba, K.; Nishimoto, I. Biophys. Res. Commun. 273, 442-447, 2000 Molecular cloining of a cyclin-like protein associated with cyclin-dependent kin	A; Residues: 1-504 <car> A; Residues: 1-504 <car> A; Cross-references: EMBL:211610; NID:91065725; PIDN:CAA77682.1; PID:91065726 C; Comment: This protein interacts with cellular transcription factors to transactiva</car></car>
A; Contents A; Accessio A; Molecule	A;Contents: Brain A;Contents: Brain A;Accession: JC7317 A;Accession: JC7317 A;Molecule type: mRNA	Cyenectus: A.map position: 0.07-0.086 C.Superfamily: herpesvirus alpha trans-inducing protein C.Keywords: DNA binding: transcription regulation
Comm	is: 1-308 CMAI> .: This protein, a cyclin-like protein, is essential for regulation of Gl-S tran	Alignment Scores: 0.803 Length: 504
C;Genetics: A;Gene: 1k3	s: :k3-1	94.00 Matches: milarity: 33.75% Conservative:

Oy 238	0y 371 AGGGCTGCGGCTGCACCG	A.Cross-references: FlyBase:Fggn0000667 A.Introns: 1161/3; 1205/1; 1283/1; 1432/3; 1489/2; 1912/3 A.Note: EG:133E12.4 Alignment Scores: 1.19 Length: 2342 Score: 92.50 Matches: 18 Bercent Similarity: 40.74% Conservative: 18 Best Local Similarity: 27.41% Mismatches: 41 Query Match: 27.41% Mismatches: 39 Ouery Match: 8.40% Conservative: 18 Best Local Similarity: 40.74% Mismatches: 39 Ouery Match: 27.41% Mismatches: 39 Ouery Match: 8.40% Conservative: 18 Description: 111
Best Local Similarity: 27.50% Mismatches: 41 Query Match: 9.09% Indels: 65 DB: 2 Gaps: 7 US-09-966-880A-7_COPY_80_676 (1-597) x JC1306 (1-504) QY 569 GGTAAGTCATCAACCTCATACAGGGCAA	ATGGCTATTTGCACCCGGCGGGTGCAGCCGCGTCTCACAGCCGGTGCAGCCGGTGCAGCCGGTGCAGCCGGTGAGGTGGTGAGGTGGTGAGGTGGTGAGGTGGTGAGGTGGT	C.Species: Mas musculus (house mouse) R.Yan, C.; Tamm, I. Proc. Natl. Acad Sci. U.S.A. 89, 8859-865, 1992 A.Title: Wolecular cloning and characterization of additional factors that bind to the in A.Reference number: A46241 A.Residue: 12.77 ctAn. A.Rocasion: A6641 A.Stetus: preliminary A.Rocasion: A6641 A.Stetus: preliminary A.Goss-references: GB:LI3610, NID:9293674; PIDN:AAA39332.1; PID:9293675 A.Note: sequence extracted from NCBI backbone (NCBIN:115299, NCBIP:115300) Alignment Scores: A.Note: sequence extracted from NCBI backbone (NCBIN:115299, NCBIP:115300) Alignment Scores: Bercent Similarity: A.Score: Bercent Similarity: Best Local Similarit

Oy 443 GGAATACTTTGTAGAAAACCATGAAACATTTCAAAGCCTGGGAAGGGCTGCATGAAA 502 11111 11 11 11 11 11 11	Percent Similarity: 41.57% Conservative: 9 Best Local Similarity: 31.46% Mismatches: 23 Query Match: 8.04% Indels: 29 DR: 5
ATTCAGTTCGTCTCCAGACAGCTTCGCCGCATCTTTG 543	09-966-880A-7_COPY_80_676 (1-597) x A38218 (1-1493)
	111 CAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGT
NESULI 13 TO4859 homolog F28A21.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999	Db 1411 GInCysProPhePheTyrAsnArgFroILeSerGlu
C.Accession: T048.09 K.S.Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A.Reference number: 215387	Qy 219 CCGCTGCTACCGCGTCACCTGGTT
A;Mocession: Tudaby A;Molecule type: DNA A;Residues: 1-839 <bev> A;Cross-references: BMBL:AL035526 A;Experimental course outlivivar Columbia: BAC clone 578821</bev>	Qy 255 CCCTGCTACGACTGTGCCGACATGTGGCCGACTTTCTGCGAGG
C, Genetics: A; Map position: 4 A; Introns: 623/3 A: Note: PSRA21 80	Qy 300GAACCCCAACCTCAGGAT 323 Db 1480 GluProProGlnProArgLysGlnGlu 1488
	RESULT 15 T02345 hypothetical protein KIAA0324 - human (fragment)
1.50 Matches: 27 1arity: 47.06% Conservative: 5 1.mllarity: 39.71% Mismatches: 33	C:Species: Homo sapiens (man) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999 C;Accession: T02345
Indels: 3 Gaps: 2	R;Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998
US-09-966-880A-7_COPY_80_676 (1-597) x T04859 (1-839)	A;Description: Sequencing of human chromosome 16p13.3.
Qy 221 GCTGCTACCGCGTCACCTGCTCGGAGCCCCTGCTACGACTGTGCCCGACATG 280 :::	A; Accession: funct: 21400; A; Accession: funct: 10246 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
Qy 281 TGGCCGACTTTCTGCGAGGAACCCCAACCTCAGTCTGAGGATCTTCACGCGCGCCTCT 340	A;Residues: 1-1791 <ric> A;Cross-references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650 C;Genetics: A;Map position: 16</ric>
ACTICIGIGAGGACCGCAAGGCTGAGGCGCTGCGGCGGCTGCACCGCGCGGG 400	A; Introns: 1610/2; 1706/2 A; Note: KIAA0324
Db 498 ProThrThrProThrProGlyGlySerProProSerSerProThrThrProSerProGly 517	Alignment Scores:
Qy 401 TGCAAATAGCCATCATGACCTTCA 424 Db 518 GlySerProProSerProSer 524	87.50 1arity: 39.80% imilarity: 30.85%
RESULT 14 A38218	Indels: Gaps:
GAP-associated protein p190 - rat C;Species: Rattus norvegius (Norway rat) C:Date: 04-War-1903 #sequiance revision 18-Nov-1904 #text channe 18-Nov-1904	US-09-966-880A-7_COPY_80_676 (1-597) x T02345 (1-1791)
C;Accession: A38218 R;Settleman, J; Narasimhan, V.; Foster, L.C.; Weinberg, R.A.	5.90 COLDANGARO CONTROLLO CARLON CONTROLLO CARLON CONTROLLO CONTROLLO CARLON CA
AsTille 3, 3,3, 153, 153, Astille 1,3, Astill	OY 530 CGAAGCTGTCTGGAGAGGAGCTGAATTTCATGCAGCCTTCCCAGGCTTTGAAAGTT 471
A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid; protein A;Residues: 1-1493 ASET> A;Note: sequence extracted from NCBI backbone (NCBIP:101780)	Qy 470CTTTCATGGTTTTCTACAAAGTATTCCAGCAGTAAAAATAATCTTTGAAGGTCATG 414
Alignment Scores: 2.83 Length: 1493	OY 413 ATGCTATTTGCACCCGGGGGGGGGGCGCGCGCGCACCCTCGGGCTCAGCCTTGCGG 354

PTGAGGTTGGGGTTCCTCGC 294	ArgSerAlaSerSerProArg 784	TAGCAGGGGTCTCAGGAGA	VSProAragivLenginara 804	* 950	rgArgArgAspArgSerGlv 824			GATAACCAAACCAAAACAAAAAAAAAAAAAAAAAAAAAA	::::: ::::: HisSerArgSerProAla 858	GGTAGGTCTCACGCCGACCCA			
353 TCCTCACAGAAGTAGAGGCGCGCGGTGAAGATCCTCAGACTGGGGTTGGGGGTTCCTCGC 294	767 ProAlaGluLysSerArgSerSerArgArgArgArgSerAlaSerSerProArg 784	AGAAAGTCGGCCACATGTCGGGCACAGTCG	785 Thr.LysThrThrSerArgGlyArgSerProSerProLysProArgGlyLenginard		805 SerArgSerArgSerArgGluLysThrArgThrThrArgArgAsgAspArgSerGlv 824	GTGAACCAGGTGACGCGGTAGCAGCGGCCAGGGTCTAGG	825 SerSerGlnSerThrSerArgArgArgGlnArgSerArgSerArgSerArgValThrard	AGGAAGAATTCCACGTGGCAGCCGTTCTTATTGCGA		125 AAGGATGTAGCACTGTCACGCCTTCACTACGTAGCACAGGTAGGT		T 65	878 o 878
353	167	293	785	246	802	245	825	185	845	125	859	65	878
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Search completed: June 14, 2003, 18:56:35 Job time: 24.1832 secs ictalurid h pseudorabie caenorhabdi

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RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Balley J., Barlow K.F., Bates K.N., Baeasley O.P.,
RA Bagguley C., Balley J., Bridgeman A.M., Buck D., Burgess J.,
RA Burill W.D., Burton J., Cardem C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Coble V. B., Cole C.G., Collier R.E., Connor R.,
RA Canroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Chanh P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gilbert J.G.R., Goward M.E., Graffam D.V., Carffiths M.N.D., Hall C.,
RA Gilbert J.G.R., Goward M.E., Graffam D.V., Carffiths M.N.D., Hall C.,
RA Hull R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
Martyn I.D., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
Martyn I.D., Mashreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Godell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,
RA Hullips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Sann R.M.,
Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
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RA Borman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                           CA1E_CHICK
CIT1_HUMAN
VEZ_HPV08
CD45_RAT
VGLD_PRVRI
AMYH_YEAST
CIC_DROME
CA1C_MOUSE
RW1_MOUSE
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A2AB_ORYAF
NU62_MOUSE
MUC1_XENLA
                                               VG50_HSVI1
IE18_PRVKA
                                                                                                                              CA14_CAEEL
AAAS_HUMAN
VGLX_HSVEB
HXA5_HETFR
YG4B_YEAST
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TR2B_HUMAN
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    NCBI_TaxID=9606;
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-MODEL-frame+_n2p.model -DEV=x1p
-Q-/cgn2_L/UG702_LX05TPC_spool_LX05966880/runat_14062003_175524_10304/app_query.fasta_1.9493
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-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0 -SGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Ray D., Ray D., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., A hang G., Chissoe S., Murray J., Miller N., Minx P., Cordes M., Du Z., Fulton E., Bentley D., Bradshaw H., Bourne S., A Hinds K., Kemp K., Latrellle P., Layman D., Ozersky P., Rohffing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J., Roff I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., A Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tahan R., Tahan R., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 LeuwetaspProaspThrPheThrPheAsnPheAsnAsnAsnAspProLeuValLeuArgArg 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 AspGlnHisMetGlyPheLeuCysAsnGluAlaLysAsnLeuLeuCysGlyPheTyrGly 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of phorbolin 3.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES FAMILY. STRONG, TO APOLIPORROTEIN B MRNA EDITING PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 TGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGC
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Mismatches:
                                                                                                                                                                                                                                                                   "The DNA sequence of human chromosome 22.";
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                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 148-382 FROM N.A.
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Query Match:
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277 CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACGGGGGG 336
                  387
                                                                                         -- AspTyrAspProLeuTyrLysGluAlaLeuGlnMetLeu 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGCGGCTG
                                                                                                                  388 CACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAAT
                                                                                                                                                                                                  347 ThrPheValTyrArgGlnGlyCysProPheGlnProTrpAspGlyLeuGluHisser
                                                                                                                                   ACTITIGIAGAAAACCAIGAAAGAACTITCAAAGCCIGGGAAGGGCTGCAIGAAAAITCA
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H., Dumanski J.P., Tommerup N., Collins J.E., Wright C.L., Dunham I., Macginnitle A.J., Davidson N.O., Cells J.E., "Fig." "Psoriasis up-regulated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed-1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 AA; 23012 MW; 42E99E0D7DF7AA14
                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                             199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aarhus/Ghent-2DPAGE; 2116; IEF.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 53-60; 112-121 AND 129-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Epidermis;
MEDLINE-99399284; PubMed-10469298;
                                                                                                                                                                                                                                                                                                                      PHB1_HUMAN STANDARD; PR
P31941; 012807;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequen
15-JUN-2002 (Rel. 41, Last annotter
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363.50
58.12%
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                                                                                   312 IleTyr----
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                163 TGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGTGGCCGACTTTCTGCGAGGGAACCCCCAACCTCAGTCTGAGGATCTTCACCGCGGGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 IleTyr------AspTyrAspProLeuTyrLysGluAlaLeuGlnMetLeu 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507
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Submitted (JUN-1996) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTDYLATE DEAMINASES
FAMILY. STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuMetAspProHisIlePheThrSerAsnPheAsnAsn-----GlyIleGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 CACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAAT
                                                                                                                                          TTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
                                                                                                                                                                                                                                                                                                                                                                                  AspGlnHisArgGlyPheLeuHisAsnGlnAlaLysAsnLeuLeuCysGlyPheTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTITIGIAGAAAACCAIGAAAGAACTITCAAAGCCIGGGAAGGGCIGCAIGAAAAITCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                           US-09-966-880A-7_COPY_80_676 (1-597) x PHB1_HUMAN (1-199)
  57
23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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43.468
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  Best Local Similarity:
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Q9UE74;
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                        Query Match:
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ID PHB2_HU
DT 16-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0CT-10-0C
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|01 ValArgAlaPheLeuGlnGluAsnThrHisValArgLeuProIlePheAlaAlaArgIle 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 TACTTCTGTGAGGACCGCAAGGCTGAGCCC-----GAGGGGCTGCGGGGCTGCAC 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITGIAGAAAACCAIGAAAGAACIIITCAAAGCCIGGGAAGGGCIGCAIGAAAAIICAGII
                                                                                                                                                                                                                                                                                                                                                                                       MetaspproaspThrPheThrPheAsnPheAsnAsnAspProLeuValLeuArgArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HisAlaAspTrpArgPheLeuAspLeuValProSerLeuGlnLeuAspProAlaGlnIle
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                                                                                                                                                                                                                                                                                                                                                     16 ATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGGCGT
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                 A54DCBC100FC26F3 CRC64;
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78
27
65
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
APOBECI.
                                  EMBL; U61083; AAD00089.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; FALSE_NEG
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
                                                                                                                 22453 MW;
                                                                                                                                                                        9.51e-23
339.00
55.26%
41.05%
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                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                               190
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                                                                                                                                                        Alignment Scores:
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                                                                                               Hydrolase.
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                                                                                                                   SEQUENCE
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124 AAAGATTATTTTACTGCTGGAATACTTTTGTA 456

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RESULT
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                                                                                                                                                                                                                                              -i- SUBUNIT: HOWODIMER (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                              Yamanaka S., Poksay K.S., Balestra M.E., Zeng G.-Q., Innerarity T.L.; "Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc motif is essential for catalytic activity, and noncatalytic auxiliary factor(s) of the editing complex are widely distributed.", J. Biol. Chem. 269:21725-21734(1994).

-I- PUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
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C->A: NONE OR LITTLE EDITING ACTIVITY.
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STRAIN-New Zealand white; TISSUE-Small intestine; MEDLINE-94342367; PubMed-8063816;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseé(isb-sib.ch).
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- COPACTOR: ZINC (BY SIMILARITY).
- SUBUNT: HOWODIMER.
- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE.
- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
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MEDLINE-94359963; PubMed-8078915;
Lau P.P., Zhu H.-J., Baldini A., Charnsangavej C., Chan L.;
"Dimeric structure of a human apolipoprotein B mRNA editing protein and cloning and chromosomal localization of its gene.";
Proc. Natl. Acad. Sci. U.S.A. 91:8522-8526(1994).
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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30-MAY-2000 (Rel. 39, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (HEPR).
APOBEC1.
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PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
METAL 61 61 ZINC (BY SIMILARITY).
SerGluTyrCysTyrCysTrpGluAsnPheVal 157
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TISSUE-Peripheral blood leukocytes;
MEDLINE-98140126; PubMed-9479499;
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EMBL; AB009424; BAA23882.1; JOINED.
EMBL; AB009425; BAA23882.1; JOINED.
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MEDLINE=94268910; PubMed=8208612;
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01-FEB-1996 (Rel. 33, Last sequ
30-MAY-2000 (Rel. 39, Last anno
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J. Biol. Chem. 270:13042-13056(1995).
-!- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
-!- COPACYOR: ZINC (BY SIMILARITY).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
S -> T (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 1).
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16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
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MEDLINE-95286585; PubMed-7768898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 CGGCGTGAGACCTACCTGTGCTACGTAGTGAAG-----AGGCGTGACAGTGCTACATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ITTICACTGGACTITGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTC 183
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                         SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 CTC---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerVal----
TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
                                                                                                                                                                                                                                                                                                                                                               ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
1CBCF9929066ABAD CRC64;
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24
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                         Přan; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
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                                                                                                                                                                                                                                                                               MGD; MGI:103298; Apobec1.
InterPro; IPR002125; dCMP/cyt_deam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                     EMBL; U21951; AAC52211.1; -. EMBL; U21947; AAC52211.1; JOINED. EMBL; U21948; AAC52211.1; JOINED. EMBL; U21949; AAC52211.1; JOINED. EMBL; U21950; AAC52211.1; JOINED. EMBL; U22262; AAC52212.1; -.
                                                                                                                                                                                                                                                                                                                                                               93 Z1
96 Z1
193 LE
27521 MW;
                                                                                                                                                                                                                                                                     AAC52214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2.75e-11
211.00
55.30%
37.12%
19.16%
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U22263; AAC52213.1;
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96
180
129 AA;
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                     EMBL; U22264;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                       FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 CGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGTGGAATTGCTCTTC---CGCTACATCTCGGACTGGGACCTAGACCCTGGCCGC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 ArgCysSerIleThrTrpPheLeuSerTrpSerProCysGlyGluCysSerArgAlalle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      883 GCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTAC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:::|||||| ||| ||| ::
| ArglysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                             Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 TGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisThrSerGlnAsnThr------AsnLys-----
                                                                                                                                                                                                                                                                             Science 260:1816-1819(1993).

-1- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF A CAA CODON FOR GLM TO A UAA CODON FOR STOP IN THE APOB MRNA.-1- COFACTOR: ZINC (BY SIMILARITY).
                                                                                                                                                                                             STRAIN-Sprague-Dawley, TISSUE-Small intestine;
MEDLINE-93289362; PubMed-8511591,
Teng B., Burant C.F., Davidson N.O.;
"Molecular cloning of an apolipoprotein B messenger RNA editing
                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
             01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (REPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIE:
W; 08766441882789B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-966-880A-7_COPY_80_676 (1-597) x ABME_RAT (1-229)
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Mismatches:
Indels:
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Matches:
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Pfam; PF00383; dcMp_cyt_deam; 1.
PR051TE; PS00903; CYT_DCMP_DEAMINASES; 1.
MRNA Processing; Hydrolase; Zinc.
fl fl zinc (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 I
27274 MW;
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198.00
47.06%
32.94%
17.98%
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                                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                NCBI_TaxID=10116;
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                                                                               APOBEC1
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RP 125

RP 127

RP 127
[2] HisHisAlaAspProArg---AsnArgGlnGlyLeuArgAspLeuIleSerSerGlyVal 139
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                                                                                                                                                                                                                                                                                                                                                             160 SerProSerAsnGluAlaHisTrpProArgTyrProHisLeuTrpValArgLeu---- 177
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                                                                                 343 TTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGGCTGCACCGCGCGGGGGTG
                                                                                                                                                                                                                                        103 CAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTGTAGAAAAC
                                                                                                                                                                                                                                                                                                        463 CATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyland K.M., Hieter P.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23B4CBD6AE26E793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-10N-2002 (Rel. 41, Last annotation update)
Kinetochore protein CTR19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    523 CAGCTTCGGCGCATCCTTTTGCCCCTGTAT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 -----TyrValLeuGluLeuTyr 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42782 MW;
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Q02732;
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CT19_YEAST
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                                                                                                                                                                                                                                                                                                                                          LeuValThrLysTyrAspThrLeuProLeuLeu-------Asn 149
                                                                                                                                                                                                                                                                                                 118 AlaIleSerAspArgLysArgValGluArgIleAsnGlyLeuThrAsnLeuGlnLysGlu 137
                                                                                                                                               64 AAGGGTCGGCGTGAGACCTACCTGTGCTAGTGAAGAGGCGTGACAGTGCTACATCC 123
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| MetAsnLeuArgLeuSerTyrLeuArgAspHisThrTyrProHisLeuGlnValSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                      124 TTTTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC---
                                                                                                                                                                                                               -------AspIleLeuGln
                                                                                                                                                                                                                                   ------CGCTGCTACCGCGTCACCTGGTTCACCTGGAGC-----
                                                                                                                                                                                                                                                                                                                      -----CCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAAC
                                                                                                                                                                                                                                                                                                                                                                 CTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTTTTACTGCTGGAATACT-----TTTGTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 AACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCAT---GAAAATTCAGTTCGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TCCAGACAGCTTCGGCGCATCCTTTTGCCCCTGTATGAG
                                                                                                      GACAGCCTCTTGATGAACCGGAGGAAGTTTCTTTACCAATTCAAAAATGTCCGCTGGGCT
                                                                                                                          AspAlaLeuLeuThrArgArgAsnThrLeuLeuGlnGluIle------
                                                                                                                                                                   ------GlnThrTyrGlnAsnIleLeuMetLysGluAsnAsnSerLysThr---
                                                                                                                                                                                                                                                 GAGGGGCTGCGGCGCCGCGGGCGGGGTGCAAATAGCCATCATGACCTTCAAAGAT
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01-APR-1993 (Rel. 25, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
Alpha trans-inducing protein (Alpha-TIF).
Bovinch herpesvirus type 1 (strain P8-2).
Viruses; AsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                  (1-369)
        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                 US-09-966-880A-7_COPY_80_676 (1-597) x CT19_YEAST
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                                                              Gaps:
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       0.412
97.50
37.33%
22.22%
8.86%
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                           Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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P30020;
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                                                  Query Match:
DB:
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ATIN_HSVBP
TATIN HSVBP
AC P30020;
DT 01-APR:
DT 01-PAR:
DE Alpha 1
OC VITUSE:
OC VITUSE:
OC NCBL_T;
RP SEQUEN
RX MEDLIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ArgSerGlySerThrArgThrArgGlyArgAlaAlaArgSerThrThrGlyArgLeuGln 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------AlaArgGlyGluProArgHisThrSerGlySerGly 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 sLysAlaArgSerGlyProAlaArgGlyGlyProGlyProSerProValArgSerGlyLe 452
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                                                                                           FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF IMMEDIATE
                                                                                                                                              PROTEIN.
                 "Sequences of the bovine herpesvirus 1 homologue of herpes simplex virus type-1 alpha-trans-inducing factor (UL48)."; Gene 119:259-263(1992).
                                                                                                                    EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro: IPRO3174; Alpha_TIF.
Pfam: PF02232; Alpha_TIF; 1.
Transcription regulation; Trans-acting factor; DNA-binding.
SEQUENCE 504 AA; 54028 MW; 0031B4B0E31FCD25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 uGlyLeuSerArgAlaArgGlySerPro----------
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44
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41
65
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Mismatches:
Indels:
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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94.00
33.75%
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PIR; JC1306; JC1306
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Best Local Similarity:
Carpenter D.E.,
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ID VE2_HPV24
AC P50770;
DT 01-0CT-1996 (
DT 01-0CT-1996 (
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Pred. No.:
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DB:
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DOMAIN
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 ACCCCGCGCGCGGTGCAGCCGCCGCGCGCCTCGGGCTTGCGGGTCCTCACAGAAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ThraspSerArgCysArgArgArgSerSerSer-----ArgGlnLysLysGln 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 TAGAGGCGCGCGGTGAAGATCCTCAGACTGAGGTTGGGGGTTCCCTCGCAGAAAGTCG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 GlyArgargalaargSerargThrargSerArgCysSerSerThrGlnThrargSerarg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 GCCACATGTCGGGCACAGTCGT----AGCAGGGGCTCCAGGAGGTGAACCAGGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 gGlyAspThrProArgGlyGlnArgGlyValSerThrSerSerArgGlyArgGly----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delius H.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                          Human papillomavirus type 24.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                        8E04B454AD44CB63 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR001866; E2_N.
Pfam; PF00508; E2_N; 1.
Probom; PD000672; E2_C; 1.
Probom; PD000678; E2_C; 1.
Probom; PG000678; E2_N; 1.
                                                                                                                                                                                                                                                                      EMBL; U31782; AAA79418.1; -. HSSP; P03122; 2BOP.
                                                                                                                                                                                                                                                                                                                                                                                                                               4.07
86.50
44.68%
33.33%
8.37%
    Regulatory protein
                                                                                                SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=37956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                          Papillomavirus
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                                                                                                                 Delius
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NU62_HUMAN
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                                                                                                                                                                                                                                                                                                                                           TISSUE—Skin, and Urinary bladder;

A Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

- I- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEAR PORE COMPLEX.

THE N-TERRINAL IS PROBABLY INVOLVED IN NUCLEOCYTOPLASMIC
TRANSPORT. THE C-TERMINAL IS PROBABLY INVOLVED IN PROTEIN-PROTEIN

INTERACTION VIA COLLED-COLL FORMATION AND MAY FUNCTION IN

ANCHORAGE OF P62 TO THE PORE COMPLEX.

THE TRANSPORTER. DURING MITOTIC CELL DIVISION, IT ASSOCIATES WITHIN

THE POLES OF THE MITOTIC SPINDLE.

THE POLES OF THE MITOTIC SPINDLE.

--- DOMAIN: CONTAINS F-X-F-G REPEATS.

CHAIN SITES PREDICTED FOR THE ENTIRE PROTEIN, AMONGST WHICH ONLY
                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                 [1] SEQUENCE FROM N.A. MEDLINE—92001039; PubMed=1915414; MEDLINE—92007939; PubMed=1915414; Carmo-Fonseca M., Kern H., Hurt E.C.; "Human nucleoporin p62 and the essential yeast nuclear pore protein NSPI show sequence homology and a similar domain organization."; Aall Biol. 55:17-30(1991).
                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                  Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Coiled coil; Repeat;
                                                                                                                                                                                                                                                                           TISSUE-Brain;
Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALA-RICH.
15 X 9 AA APPROXIMATE REPEATS.
NU62_HUMAN STANDARD, PRT; 522 AA. P37138; Q981243; Q981243; Q9812194 (Rel. 30, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nuclear pore glycoprotein p62 (62 kDa nucleoporin).
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EMBL; BC003663; AAH036631;
EMBL; BC014842; AAH144211;
GlycoSulteDB; P31198;
Genew; HGNC:8066; NUP62.
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Polymorphism. 9 288
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1163
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                                                                                                                                       NCBI_TaxID=9606;
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REPEAT
REPEAT
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489
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|IeAlaThrAlaProThrSerSerAlaThrThrGlyLeuSerLeuCysThrProValThr 244
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                                                                                                                                                                                                                                                                                                                                                           ATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGACCTAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlyThrSerThrThrThrSerThrAlaAlaThrAlaThrAlaThrThrThrThrThrSer 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerThrThrGlyPheAlaLeuAsnLeuLysProLeuAlaProAlaGlyIleProSer 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCCTGCGGCGGCTGCACGCG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 CCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTACTGCTGGAATACTTTTG 454
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                                                                                                                                                                                                                                                                      -----TCACCTGGTTCACCT
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| PheThrProAlaThrProAlaAlaThrThrAlaGlyAlaThrGlnProAlaAlaProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCTCAGTCTGAGGATCTTCA-------CCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AAAGCCTGGGAA----
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15.
COILED COIL (POTENTIAL).
0-LINKED (GLCNAC) (BY SIMILARITY).
0-LINKED (GLCNAC) (BY SIMILARITY).
A -> S (IN DBSNP:2290772).
T -> S (IN REF. 3; AAH14842).
SG -> RA (IN REF. 1).
E -> Q (IN REF. 1).
E -> V (IN REF. 1).
E -> V (IN REF. 1).
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56
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27
89
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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234
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287
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                                          DOMAIN
CARBOHYD
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 TTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGCGGCGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| :::||| :::|||
PheSerPheLeuGluAspLysPheThrHisLeuAspTyrValSerAspValLeuIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AspAlaSerSerLeuHisLeuLeuArgPhePheLeuHisAspTyrTrpAsnSerPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AACGCTGCCACGTGGAATTGCTCTTC-----CTCCGCTACATCTCGGACTGGGACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 GACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCC-----TGGAGCCCCTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 GACTGTGCCCGACATGTGGCCGGACTTTCTGCGGGGAACCCCCAACCTCAGTCTGAGGATC
                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Myrtales; Myrtaceae; Kunzea.
                                                                                                                                                                                                                                                                   O'Brien M.M., Wilson P.G., Quinn C.J.;
Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
--- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TTTGGTTATCTTCGCAATAAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGAC-
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Matches:
Conservative:
Mismatches:
Indels:
                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable intron maturase (Maturase K).
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                   503
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; MatK_N; 1.
                                                                                                                                   Kunzea baxteri (Scarlet kunzea).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast; mRNA processing.
SEQUENCE 503 AA; 60203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.59
85.00
41.43%
25.00%
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                   MATK_KUNBA
Q9TKC0;
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MATK_KUNBA
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::: ::: ||||||| |||||| TyrAsnSer-----PheLeuArgAsn 225
                                                                                                    226 GlnSerSerHisLeuArgSerThrSerSerGlyIlePhe***GluArgIleTyrPheTyr 245
                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SON protein (SON3) (Negative regulatory element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1)
(BASS1) (Protein (210:150).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogal T., Sugano S.; "NEDo human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Transcription repression of human hepatitis B virus genes by negative
                                                          385 -----CTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 11 transcription map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99397452; PubMed-10470851;
Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun C.-T., Lo W.-Y., Wang I.-H., Lo Y.-H., Shiou S.-R., Lai C.-K., Ting L.-P.,
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ϊ.
                                                                                                                                                                                    SON_HUMAN STANDARD; PRT; 2426 AA.
P18583; 095981; Q9UPY0; Q14120; 014487; Q9UKP9; Q9H7B1; Q9P070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.; "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21564202; PubMed-11707072;
Weymond A., Friedli M., Neergaard Henrichsen C., Chapot F.,
Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M.,
Antonarakis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casadei R., Strippoli P., D'Addabbo P., Canaider S., Lenzi Vitale L., Giannone S., Carinci P., Zannotti M.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS A; B; C; D; E AND F).
                                                                                                                                                                                                                                                                                                                                                                             SON OR NREBP OR DBP5 OR C210RF50 OR KIAA1019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 437-2426 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory element-binding protein/SoN.";
J. Biol. Chem. 276:24059-24067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-689 FROM N.A. (ISOFORM H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21316479; PubMed-11306577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-130 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 78:46-54(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rISSUE-Smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrssue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE-Liver
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Bliskovskii V.V., Kirillov A.V., Zakhariev V.M., Chumakov I.M.;
"The human son gene: the large and small transcripts contains various
                                                                                         SON and
this gene
                                                                                                                                                                                                                                                                                                                                                     "Coding part of the son gene small transcript contains four areas of complete tandem repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CAUTION: ISOFORM F SEQUENCE FROM REF. 10 DIFFERS FROM THAT SHOWN
                                                                                                                                                                                                                                                                                                       TISSUE-Placenta;
MEDLINE-93062884; PubMed-1435773;
Bliskovskii V.V., Berdichevskii F.B., Tkachenko A.V., Belova M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1692-2175 FROM N.A. (ISOFORM A).
MEDLINE-89039788; PubMed-3054499;
Berdichevskii F.B., Chumakov I.M., Kiselev L.L.;
"Decoding of the primary structure of the son3 region in human genome: identification of a new protein with unusual structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DOMAIN: Contains 8 types of repeats which are distributed in 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
-:- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAI
-:- CAUTION: ISOFORM A SEQUENCE FROM REF. 7 DIFFERS FROM THAT SHOWN
DUE TO A FRAMESHIFT.
                            SEQUENCE OF 554-2426 FROM N.A. (ISOFORM A).
MEDLINE-92049296; PubMed-1944255;
Chumakov I.M., Berdichevskii F.B., Sokolova N.V., Reznikov M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: Colocalizes with the pre-mRNA splicing factor
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1145-2426 FROM N.A. (ISOFORM F).
MEDLINE-93048367; PubMed-1424986;
Mattioni T., Hume C.R., Konigorski S., Hayes P., Osterweil Z.,
                                                                         Prasolov V.S.;
"Identification of a protein product of a novel human gene in the biological effect upon administering a changed form of into mammalian cells.";
MOI. Biol. (MOSK) 25:731-740(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA clone for a novel nuclear protein with DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1939-2426 FROM N.A. (ISOFORM J).
                                                                                                                                                                   SEQUENCE OF 709-1079 FROM N.A. (ISOFORM I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology with DNA-binding proteins.";
Mol. Biol. (Mosk) 22:794-801(1988).
                                                                                                                                                                                                                                                              Mol. Biol. (Mosk) 26:807-812(1992).
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                                                                                                                                                                                                                                                                                         SEQUENCE OF 1009-1131 FROM N.A.
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Res. 6:197-205(1999).
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                                                                                                                                                                                                                                              -terminal sequences.
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    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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There are no restrictions on
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3 X 11 AA TANDEM REPARS C.
P-P-[TME]-[MTG].
4 X A TANDEM REPEATS OF V-L-E-SS-[AVT]-VT.
7 X 7 AA REPEATS OF P-S-R-S-R-[TS].
                                                                                                                                                                                                                                                                                                         17 X 10 AA TANDEM REPEATS OF L-A-[ST]-
[NSG]-[TS]-MDSQM.
II X 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
[LI][AG][QHP].
14 X 6 AA REPEATS OF [ED]-R-S-M-M-S.
                                                                                                                                                                                                                                             Pfam; PF00035; dsrm; 1.
Pfam; PF01585; G-patch; 1.
PROSITE: PS50137; DS. RBD; 1.
PROSITE: PS50174; G-PATCH; 1.
RNA-binding; DNA-binding; Nuclear protein; Repeat;
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Matches:
Conservative:
Mismatches:
Indels:
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European Bioinformatics Institute.
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                                                         X63753; CAA45282.1; ALT_FRAME M36428; AAA36624.1; -.
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AF380181; AAL34499.1; --
AF380183; AAL34500.1; --
AF380184; AAL34501.1; --
AF380184; AAL34502.1; --
AF435977; AAL30810.1; --
K63751; CAC69885.1; --
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InterPro; IPR000467; G_patch.
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Query Match:
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 $US-09-966-880A-7_COPY_80_676$ (1-597) x SON_HUMAN (1-2426)

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                                        521 CTGGAGAGACGAACTGAATTTTCATGCAGCCCTTCCCAGGCTTTGAAAGTTCTTTCATGG 462
                                                                                                                       461 TTTTCTACAAAAGTATTCCAGCAGTAAAAATAATCTTTGAAGGTCATGATGGCTATTTGC 402
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MEDLINE=89071743; PubMed=3200844;
D'Onofrio M., Starr C.M., Park M.K., Holt G.D., Haltiwanger R.S.,
Hart G.W., Hanover J.A.;
"Partial chanover J.A."
"Partial chan sequence encoding a nuclear pore protein modified by O-linked N-acetylglucosamine.";
Proc. Natl. Acad. Sci. U.S.A. 85:9595-9599(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91268076; PubMed=2050692;
D'Onofrio M., Lee M.D., Starr C.M., Miller M., Hanover J.A.;
"The gene encoding rat nuclear pore glycoprotein p62 is intronless.";
J. Biol. Chem. 266:11980-11985(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                SEQUENCE FROM N.A.
STRAINE-Fischer; TISSUE-Thyrold;
MEDLINE-9027705; PubMed-2190987;
Starr C.M., D'Onofrio M., Park M.K., Hanover J.A.;
"Primary sequence and heterologous expression of nuclear pore glycoprotein P62.";
J. Cell Biol. 110:1861-1871(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TICACTACGTAGCACAGGTAGGTCTCACGCCGACCCTTAGCCCAGCGG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear pore glycoprotein p62 (62 kDa nucleoporin).
NUP62.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                         *** MEDLINE-95151751; PubMed-7849028; ALDLINE-95151751; PubMed-7849028; ALDLINE-95151751; PubMed-7849028; ALDLINE-95151751; PubMed-7849028; ALDLINE-95151751; PubMed-784028; ALDLINE-95151751; PubMed-784028; ALDLINE AND AND ASSENTIAL COMPONENT OF THE NUCLEAR PORE COMPLEX. THE N-TERMINAL IS PROBABLY INVOLVED IN NUCLEOSYTOPLASMIC TRANSPORT. THE C-TERMINAL IS PROBABLY INVOLVED IN PROTEIN-PROTEIN INTERACTION VIA COLLED-COLL FORMATION AND MAY FUNCTION IN ANCHORAGE OF P62 TO THE PORE COMPLEX. CANCHORAGE OF P62 TO THE PORE COMPLEX. CHE SUBCELLUIAR LOCATION: CENTRAL REGION OF THE NUCLEAR PORE, WITHIN THE POLES OF THE MITOTIC SPINDLE. THE POLES OF THE MITOTIC SPINDLE. CHE ODMAIN: CONTAINS F-X-F-G REPEATS.
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O-LINKED (GLCNAC).
NG -> FR (IN REF. 3).
BOF02F6BF6C0816E CRC64;
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Mismatches:
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EMBL; X52583; CAA36813.1; -.
EMBL; M62992; AAA41789.1; -.
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PIR; A35596; A35596.
GlycosuitedB: P17955; ---
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Best Local Similarity:
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rakawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Rakawai T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Radawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.S., Sizuki R., Tomita M., Wagner L., Washlo T.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Radota K., Marchioni L., Mashima J., Mombaerts P.,
Lyons P., Marchioni L., Mashima J., Mombaerts P.,
Rotone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Warrencon I annotation of a full-length mouse CDNA collection.";
Warrencon and annotation of a full-length mouse cDNA collection.";
277 ThrThrThrThrThrThrThrAlaSerThrSerSerSerThrThrThrThr-GlyPh 296
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                                                        ----CCGCAAGGCTGAGCCCGAGGGCCTGCGGCGGCCTGC
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                                                                                                                                STRAIN=129/Sv;
MEDLINE=20408886; PubMed=10950926;
WFDINE=20408886; PubMed=10950926;
Wynn S.L., Fisher R.A., Pagel C., Price M., Liu Q.Y., Khan I.M.,
Zammit P., Dadrah K., Maznai W., Kessling A., Lee J.S., Buluwela L.;
"Organization and conservation of the GART/SON/DONSON locus in mouse and human genomes.";
Genomics 68:57-62(2000).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-Hippocampus, Small intestine, and Tongue; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 TTCGGCGCATCCTTTTGCCCCTGTATGAGGTTGATGACTTA 567
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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P-S-R-R-R-S-R-S-V-

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1978 ArgSerArgSerAlaValArgArgArgSerPheSerIleSerProValArgLeu---- 1995
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3-2 (APPROXIMATE).
3 X TANDEM REPEATS OF [ST]-P-[VLI]-R-[RL]-[RK]-[RK]-S-R.
G-PATCH.
                                                                                                                              MISSING (IN ISOFORM 2).
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                                                                                                                      -> F (IN ISOFORM 2)
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2-6.
2-7 (APPROXIMATE).
2 x 19 AA REPEATS O
V-R-R-R-S-F-S-I-S.
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Mismatches:
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Matches:
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Job time: 15.4884 secs
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1-12.
1-14.
3 x 11 AA TANDEM REPATS OF P-L-P-E-E-
P-P-[TME]-[MTG].
7 x 7 AA REPEATS OF P-S-R-S-R-[TS].
      sequence: 5'-6A[GT]AN[CG][AG]CC-3'. Might protect cells from apoptosis. Might be involved in pre-mRNA splicing (By similarity). SUBCELIGIAR LOCATION: Nuclear (By similarity).
ALTERNATUS PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
TISSUE SPECIFICITY: Widely expressed.
DOMAIN: Contains 8 types of repeats which are distributed in 3
                                                                                               -i- SIMILARITY: CONTAINS 1 G-PATCH DOMAIN.
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 x 10 AA TANDEM REPEATS OF L-A-[ST]-
[NSG]-[TS]-MDSQM.
Il x 7 AA TANDEM REPEATS OF [DR]-P-Y-R-
[LI][AG](QHP).
14 X 6 AA REPEATS OF [ED]-R-S-M-M-S.
 FUNCTION: Transcriptional repressor. Binds to the consensus DNA
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InterPro; IPR001159; DS_RBD.
InterPro; IPR000467; G_patch.
Pfam; PF001585; G-patch; 1.
SMART; SW00443; G-patch; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50137; DS_RBD; 1.
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BAB31659.1; -...
BAB31536.1; -..
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AAF23120.1;
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EMBL; AKO08256; BAB25562.1;
MGD; MGI:98353; Son.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE-20460541; PubMed=11007475;
REVY P., Muto T., Levy Y., Geissmann F., Plebani A., Sanal O.,
Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,
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Copyright (c) 1993 - 2003
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTGGGAAGGGCTGCATGAAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATCCTT
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                                causes
                        "Activation-induced cytidine deaminase (AID) deficiency causes autosomal recessive form of the Hyper-IgM syndrome (HIGM2)."; Cell 102:565-575(2000).
                                                           TISSUE-B-CELL;
A Strausberg R.;
L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AB040431; BAB12721.1;
R EMBL; AB040435; BAB12720.1;
DR EMBL; BC006296; AAH06296.1;
DR InterPro; IPR02125; GCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DBAMINASES; UNKNOWN_1.
SEQUENCE 198 AA; 23953 MW; 3C27BB143DB184A9 CRC64;
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Matches:
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RP SEQUENCE FROM N.A.
RX MEDLINE-99303612; PubMed-10373455;
RA Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
RA Davidson N.O., Honjo T.;
RT Davidson N.O., Honjo T.;
RT "Specific expression of activation-induced cytidine deaminase (AID), a
RT novel member of the RNA-editing deaminase family in germinal center B
RI J. Biol. Chem. 274:18470-18476(1999).
DR RMD: MGI:1342279; Aho41793.1; -.
DR MGD: MGI:1342279; Aicda.
DR NGD: MGI:1342279; Aicda.
DR NGD: MGI:1242279; Aicda.
DR NGO: MGI:1342279; Aicda.
DR NGO: MGI:1342279; Aicda.
DR NGO: MGI:1342279; Aicda.
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Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;
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          Last sequence update)
Last annotation update)
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Mismatches:
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Matches:
01-NOV-1999 (TrEMBLrel. 12, Last sequen 01-MAR-2002 (TrEMBLrel. 20, Last annots Activation-induced cytidine deaminase.
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145 CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
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GlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGlnAspLeuSerGlyArg
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                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                      79C656F580A40554 CRC64;
                                                                                                            Q9Y555 PRELIMINARY, PRT; 204 AA. Q9Y555, 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-NOV-1999 (TrEMBLrel. 21, Last annotation update) BK150C2.3 (PLEMBLrel. 21, Last annotation update) BK150C2.3 (Putative novel protein similar to APOBECI MRNA editing protein) and Phorbolin) (Fragment).
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204
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Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ dat
EMBL; ALO2318; CAB45271.1; -.
Interpro; IPR00125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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Matches:
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---AspAspGlnGlyArgCysGlnGlvGlyLeuArgThrLeuAlaGluAlaGlyAlaLys
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                                                                                                                                                                                       Huang C., Qian B., Tu Y., Gu W., Wang Y., Han Z., Chen Z., "Novel genes expressed in hematopoletic stem/progenitor cells from Myelodysplastic Syndromes patient.";
Submitted (SEP-1999) to the EMBE/GenBank/DDBJ databases.
                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                        TISSUE-JA...,
Strauberg R.;
Strauberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044268 AAH24268.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                          Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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83
31
59
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                                               01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
MDS019 (Phorbolin-like protein MDS019).
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Matches:
Conservative:
Mismatches:
Indels:
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Mammalia; Eutheria; Primates;
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390.00
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                                                                                                              Homo sapiens (Human)
                                                                                                                                                                           SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                                    NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
        540
                  CTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011739; AAH11739.1; -.
InterPro; IPR002125; dGMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 190 AA; 22827 WW; DA0584EF75C91CF0 CRC64;
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Mismatches:
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367.50
58.52%
44.89%
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                                                                 PRELIMINARY;
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01-DEC-2001 (TrEMBLrel.
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145 CTTCGCAAT-----AAGAACGGCTGCCACGTGGAATTGCTCTTCCTCGCTAC 192
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
In Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoietic stem/progenitor cells from the genes expressed in hematopoietic stem/progenitor cells from Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165520; AAF86650.1;
InterPro: IPR002125; GCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINNSES; UNKNOWN_1.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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354.00
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                                  01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Phorbolin I protein.
PRELIMINARY;
                                                                                                                                    Homo sapiens (Human)
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91 TACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 TGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 CysSerLeuSerGlnGluGlyAlaSerValLysIleMetGlyTyrLysAspPheValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITCITIACCAATICAAAAAIGTCCGCTGGGCTAAGGGTCGGCGTGAGCTACCTGTGC
                                                                                                                                                  Hypothetical 46.6 kba protein.
Hypothetical 46.6 kba protein.
Hypothetical (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC017022; AAH17022.1; -. InterPro; IPR002125; dCMP/cyt_deam. PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 GAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94C7253BDCC85B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            386
71
27
71
71
5
                                                     096AK3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
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Matches:
Conservative:
Mismatches:
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                               PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 386 AA; 46598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.71e-25
336.50
56.32%
40.80%
30.56%
                             PRELIMINARY:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       TISSUE-UTERUS;
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                             Q96AK3
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Q9Y4V1
ID Q9Y4'
AC Q9Y4'
DT 01-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .33 GACTITGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ACCTCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAAC 303
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80 PheHisAspLysValLeuLysValLeuSerProArgGluGluPheLysIleThrTrpTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 CCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 GAGCCCGAGGGCTGCGCGGCTGCACCGCGCGGGGTGCAAATAGCCATCATGACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 Gln---GlnAsnLeuCysArgLeuValGlnGluGlyAlaGlnValAlaAlaMetAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 TGGGAAGGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCGATCCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ITGATGAACCGGAGGAAGTITCTTTACCAATTCAAAAATGTCCGCTGGGCTAAGGGTCGG
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                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin
                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003314; AA4003314.1; ...
MGD: MGI:1931111; BC0003314.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE: PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 429 AA; 51017 MW; BE44D01380AD7F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429
71
36
72
     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 51.0 kDa protein.
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Conservative:
Mismatches:
Indels:
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429 AA
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  PRT;
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349.00
58.47%
38.80%
  PRELIMINARY;
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                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Best Local Similarity:
Q99J72;
Q99J72;
01-JUN-2001
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Q9Y235;
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                                                                                                                                                                                                                                                                                                                                                                     258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ494G10.1 (Novel protein similar to Phorbolin 1 and APOBEC1
(Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1))
                                                                                                                              Ramsay H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C77CB711DDAAA9C0 CRC64;
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65
24
40
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Last annotation update)
                                                                                                                                                  EMBL; AL078641; CAB45659.1; -.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                            AA; 16075 MW;
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315.50
66.42%
48.51%
28.66%
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                                                                                                                   SEQUENCE FROM N.A.
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                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                           SEQUENCE 139
                                                                                                                                                                                                                                                 Percent Similarity:
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                                            (Fragment)
DJ494G10.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 ACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG-------GGGCTG
             Liao W., Hong S.H., Chan B.H., Rudolph F.B., Clark S.C., Chan L.; "APOBEC-2, a cardiac- and skeletal muscle-specific member of the eyildine deaminase supergene family."; Biochem. Biophys. Res. Commun. 260:398-404(1999).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DJ34B21.2 (Putative novel protein similar to PART of APOBEC1 (PHORBOLIN 1, apolipoprotein B mRNA editing protein)).
HOMO sapiens (Human).
                                                                                                       MGD; MGI:1343178; Apobec2.
SEQUENCE 224 AA; 25660 MW; 75F98BC2CF2EBE0A CRC64;
                                                                                                                                                                                  224
65
26
74
12
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MEDLINE-99333690; PubMed-10403781;
                                                                                                                                                                            1.96e-19
278.00
51.41%
36.72%
25.25%
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Best Local Similarity:
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                                                                                                                                                                  Alignment Scores:
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121
14309 MW;
                                                           Matthews L.;
Submitted (DEC-1999) to the EMBL; AL022318; CAB45273.1;
NON_TER
                                                                                                                                                   1e-18
270.50
60.00%
45.83%
24.57%
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   Eukaryota; Metazoa;
               Eutheria;
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121 AA;
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                                                SEQUENCE FROM N.A.
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                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                    72 TyrValValGluAlaGlnGlyLysGlyGlyGlyGlnValGlnAlaSerArgGlyTyrLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC
                                                                                             Chan L.;
                                                                                         Liao W., Hong S. H., Chang B. J., Rudolph F.B., Clark S.C., Chan "APOBEC-2, a cardiac- and skeletal muscle-specific member of the cytidine deaminase supergene family.";
Biochem. Biophys. Res. Commun. 260:398-404(1999).
EMBL; AL031778; CAB4440.1; -.
EMBL; AF161698; AAD45360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AspileGluAsnPheLeuTyrTyrGluGluLysLeuAlaAspileLeu 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O99553;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK150C2.10 (Putative novel Phorbolin 1 like protein) (Fragment).
              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 GGGCTGCATGAAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATCCTT
              of
          "APOBEC-2, a cardiac and skeletal muscle specific member cytidine deaminase supergene family."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           CA0905AFAA8C8FA1 CRC64
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64
25
76
12
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Conservative:
Mismatches:
Indels:
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                                                                   TISSUE-HEART;
MEDLINE-99333690; Pubmed-10403781;
                                                                                                                                                                          224 AA; 25703 MW;
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274.00
50.28%
36.16%
24.89%
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Best Local Similarity:
Query Match:
                                                        SEQUENCE FROM N.A.
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Peck A.;
"APOBEC-2,
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09Y553
1D 09Y55
DT 01-NO
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DT 01-DE
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DF BK150
OS HOMO
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181 TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG 240
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45276.1; -InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                EMBL/GenBank/DDBJ databases
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BK150C2.6 (Putative novel protein similar to APOBEC1
BK150C2.6.
BK150C2.6.
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55
17
47
                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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Indels:
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Search completed: June 14, 2003, 18:47:43
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                                                                                                                                      282
                                                                                                                                                                             342
                                                                                                                                                                                                            343 TTCTGTGAGGACCGCAAGGCTGAGGCGCTGCGGCGCGCTGCACCGCGCCGGGGTG 402
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                                                                                                                                          226 TACCGCGTCACCTGGTTCACCTCCTGGAGCCCCTGCTACGAC-----TGTGCCCGACAT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 TACTICIGIGAGGACCGCAAGGCIGAGCCC-----GAGGGGCTGCGGCGGCTGCAC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 CGCGCCGGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACT 450
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                                                                                                                                                                     283 GCCGACTITCIGCGAGGGAACCCCAACCICAGICIGAGGAICTICACCGCGCGCCCTCIAC
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67 TyrPheTrpAspThrAspTyrGln---GluGlyLeuArgSerLeuSerGlnGluGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGCCGACTITCTGCGAGGGAACCCCAACCTCAGTCTGAGGATCTTCACCGGGGGCGCTC
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                                                                                                                                                                                                                                                  103 CAAATAGCCATCATGACCTTCAAAGATTATTTTACTGCTGGAATACTTTTGTA 456
                                                                                                                                                                                                                                                               Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BK15GC2.1 (Putative novel Phorbolin 1 like protein) (Fragment).
BK15GC2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45269.1; -.
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51
20
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   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                  US-09-966-880A-7_COPY_80_676 (1-597) x Q9X550 (1-103)
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Mismatches:
Indels:
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Matches:
                                                     Gaps:
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1.99e-17
257.50
63.27%
50.00%
23.39%
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251.00
64.55%
46.36%
22.80%
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Best Local Similarity:
Ouery Match:
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Best Local Similarity:
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TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTT 510
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77 PheValAspHisGlnGlyCysProPheGlnProTrpAspGlyLeuAspGluHisSerGln 96
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK15CC2-9 (Putative novel Phorbolin 1 like protein) (Fragment).
BK15CC2-9.
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48
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119
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Conservative:
Mismatches:
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                                                                                                                    511 CGTCTCTCCAGACAGCTTCGGCGCATCCTT
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240.50
54.92%
39.34%
21.84%
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Query Match:
DB:
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Job time : 40.6063 secs

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Perfect score: Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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Sequence 3, Appli
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Sequence 4, Appli
Sequence 11, Appli
Sequence 11, Appli
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Sequence 7, Appli
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Sequence 137,
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Sequence 5, A
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US-08-818-111-137
US-09-056-556-142
US-09-072-596-137
US-09-092-315-5
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US-09-627-650B-1
US-09-436-063C-1
US-09-436-063C-7
US-09-627-650B-7
US-09-627-650B-3
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GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: GOLI, SULYA K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                          US-09-092-315-3
US-08-922-865-2
US-09-510-949-2
US-09-041-886-19
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US-09-206-899-19
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US-09-103-429A-3
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US-07-906-349A-6
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                                                                    US-08-816-241-5
US-09-040-482-5
US-09-128-395-5
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FILING DATE: Filed Herewith
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Patent No. 5804185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 CLASSIFICATION: 435
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-08-816-241-1
                                                                                                                        \begin{array}{c} 888888\\ 88.0289\\ 8.0289\\ 8.0289\\ 8.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289\\ 9.0289
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Sequence 1,
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Sequence 1,
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                                                                                                                        June 14, 2003, 18:13:03; Search time 5.75003 Seconds
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1 atggacagcctcttgatgaa......ttcgtactttgggactttga
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3: /cgn2_f/ptodatz/l/iaa/6A_COMB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-816-241-1
US-09-128-395-1
US-09-040-482-1
US-08-687-895-3
US-08-687-895-3
US-09-040-482-3
US-09-040-482-3
US-09-128-395-3
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US-09-128-395-4
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Ygapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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369.5 369.5 271 271 245 245 245 245 245 216.5 216.5

Score

80

Result

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Score:
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                                                                                                                                                                                                                                                                                                              37 PhethrvalGluGlyIleLysArgArgSerValValSerTrpLysThr-----GlyVal
                                                                                                                                                                                                                                                                                                                                                      433 ITITACTGCTGGAATACTTTTGTAGAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 CIGCATGAAATTCAGTTCGTCTCCCAGACAGCTTCGGCGCATCCTT 540
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| 114 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
                                                                                                                                                                                                                 US-09-966-880A-7_COPY_80_676 (1-597) x US-08-816-241-1 (1-190)
                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TILE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: CA
STATE: CA
COUNTRY: USA
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                   3.67e-35
369.50
58.52%
44.89%
                                                                         LIBRARY: PROSTUT09
CLONE: 1646823
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COMPUTER READABLE FORM:
                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                     Alignment Scores:
                                                                                              US-08-816-241-1
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DB:
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91 TACGTAGTGAAG-----AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTAT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0239 I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 annino acids
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369.50
58.52%
44.89%
33.56%
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                                                                                                                                                                                                                                                                                                                                                      LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                       CLASSIFICATION:
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Best Local Similarity:
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CLONE: 1646823
                                                                                                                                                                              FILING DATE:
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439 TGCTGGAATACTTTTGTAGAAACCATGAA------AGAACTTTCAAAGCCTGGGAA 489
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                                                     328 ACCGCGCCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAG-
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
ATTLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
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Mismatches:
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Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
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REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09040482
Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 3174 Porter Drive
Palo Alto
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271.00
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24.61%
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MEDIUM TYPE: Diskette
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Best Local Similarity:
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| 111 PheAspProAlaLeuArgTyrAsnValThrTrpTyrValSerSerProCysAlaAla 130
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174 LeuLysThrAsnPheArgLeuLeuLysArgArgLeuArgGluSerLeu 189
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                                                                                                               APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOCTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                Sequence 1, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 amino acids
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                                                                                                                                                                                                                                                                                                     94304
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                                              US-08-687-895-1
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LENGTH: 116 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 IGCTGGAATACTITIGTAGAAAACCATGAA------AGAACTITCAAAGCCTGGGAA 489
                                                                                                                                                                     .51 AATAAGAAC---GGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACTGGGAC 207
                                         379 CGGCGCCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 GGGCTGCATGAAATTCAGTTCGTCTCTCCAGACAGCTTCGGCGCATC 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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62 AspAlaGlyAlaGlnValSerIleMetThrTyrAspGluPheGluTyrCysTrpAspThr
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Conservative:
Mismatches:
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Patent No. 5804185
GENERAL INFORMATION:
APPLICANT GOLI, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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STREET: 3174 Porter Drive
CITY: Palo Alto
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245.00
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                   LIBRARY: GenBank
CLONE: 436941
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Best Local Similarity:
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451 TTTGTAGAAAACCATGAAAGAACTTTCAAAGCCTGGGAAGGGCTGCATGAAAATTCAGTT 510
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 CGTCTCTCCAGACAGCTTCGGCGCATCCTT 540
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STREET: 3174 Porter Drive
                                                                                                                                                      PF-0109 US
CURRENT APPLICATION DATA:
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
FILING DATE:
                                                                                                  ATTORNY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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245.00
61.82%
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                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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                                            FILING DATE:
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
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                                          PF-0239 US
      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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245.00
61.82%
46.36%
22.25%
                                                                                                                                 LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                             STRANDEDWESS: Single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 436941
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MEDIUM TYPE: Diskette
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APPLICANT: Hillman, Jennifer
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Matches:
Conservative:
Mismatches:
                                                         OPERATING SYSTEM: DOS
SOFTWARE: PESSESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
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NAME: Billings, Lucy J.
REGISTRATION NUBBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: alinear
TYPE: ALINEANESS: Single
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                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
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Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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245.00
61.82%
46.36%
22.25%
              COMPUTER READABLE FORM:
                                        COMPUTER: IBM COMPOSERATING SYSTEM:
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                                                                                                                        CLASSIFICATION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                 FILING DATE:
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Pred. No.:
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TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
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Matches:
                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTONNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELEPAN: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acids
STRANDEDNESS: single
STRANDEDNESS: single
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COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
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216.50
59.52%
34.92%
19.66%
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CLONE: 1177798
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Best Local Similarity:
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IMMEDIATE SOURCE:
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- 150
                  319 AGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTG 378
                                        379 CGGCGCCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTAC
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                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
PRING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09040482; Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                         439 TGCTGGAATACTTTTGTA 456
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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19.66%
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Best Local Similarity:
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MOLECULE TYPE:
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                                                            Sequence 4, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
ITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Palo Alto
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J.
RESISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
152 CysTrpArgAsnPheval 157
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TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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216.50
59.52%
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STRANDEDNESS: si
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Query Match:
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                                                 US-08-816-241-4
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                                  RESULT 10
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379 CGGCGGCTGCACCGCGCGCGGGTGCAAATAGCCATCATGACCTTCAAAGATTATTTTTAC 438
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                                                                                                                                                                          33 ArgLysGluAlaCysLeuLeuTyrGluIleLysTrpGlyMetSerArgLysIleTrpArg
                                                                                                                                                                                                                                                                                     199 GACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
                                                                                                                                             103 AGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTTATCTTCGC
                                                                                                          US-09-966-880A-7_COPY_80_676 (1-597) x US-09-128-395-4 (1-236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street, Suite 800
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42
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                    Conservative:
Mismatches:
                                                        Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08158682A Patent No. 5434058 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION NUMBER: US/08/158, FILING DATE: CLASSIFICATION: US/08/158, TILING DATE: CLASSIFICATION: CLASSIFICATION: CLASSIFICATION: NAME: CCOlley, Ronald B. REGISTATION UNMBER: 27,187 REPERENCE/DOCKET UNMBER: ARC: TELEPHONE: (312) 744-0090 TELEPHONE: (312) 245-4961 INFORMATION: OF SECTION FOR SECTION OF 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 TGCTGGAATACTTTTGTA 456
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| 152 CysTrpArgAsnPheVal 157
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LENGTH: 236 amino acids
TYPE: amino acid
216.50
59.52%
34.92%
19.66%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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STATE: Illinois
COUNTRY: IIS'
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            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                      GACTGGGACCTAGACCCTGGCTGCTACCGCGTCACCTGGTTCACCTCCTGGAGCCCC
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Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: DOS
FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/09/128,395
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                                                                                                                                                                                                                                                                                                                                                                                                          152 CysTrpArgAsnPheVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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TOPOLOGY: linear
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32.94%
17.98%
                             LENGTH: 229 amino acids TYPE: amino acid
  INFORMATION FOR SEQ ID NO:
               SEQUENCE CHARACTERISTICS:
                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide US-08-158-682A-2
                                                        single
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                         TYPE: amino a STRANDEDNESS:
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Patent No. 5434058
GENERAL INFORMATION:
APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION:
APOLICANTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
                                                                                                                                              US-09-966-880A-7_COPY_80_676 (1-597) x US-08-158-682A-4 (1-236)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
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STREET: 321 No. 5434058th Clark Street, Suite
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Mismatches:
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Matches:
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NAME: COOLDEY, RODBID B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECHONE: (312) 744-0090
TELEPHONE: (312) 245-4961
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ADDRESSEE: ARNOLD, WI
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STATE: Illinois
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Best Local Similarity:
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33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg
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321 No. 5550034th Clark Street, Suite
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APPLICANT: Teng, BaBie
APPLICANT: Davidson, Nicholas O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolipoprotein B RNA Edit
TITLE OF INVENTION: Composition and Method
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5550034th Clark Street, Suii
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Patent No. 5550034
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101 ThrGluPheLeuSerArgTyrProHlsValThrLeuPheIleTyrIleAlaArgLeuTyr 120
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33 ArgLysGluThrCysLeuLeuTyrGluIleAsnTrpGlyGlyArgHisSerIleTrpArg 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-966-880A-7_COPY_80_676 (1-597) x US-08-015-203-2 (1-229)
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
RPELICATION NUMBER: US/08/015,203
FILING DATE: 19930209
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REFERENCE/DOCKET NUMBER: ARCD: 069
TELECHONICATION INFORMATION: TELEPHONE: (312) 245-4961
INFORMATION FOR ESQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 229 amino acids STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single
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Search completed: June 14, 2003, 18:59:22

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US-10-184-634-103
US-10-184-644-65
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Patent No. US20020164743a1
GENERAL INFORMATION:
APPLICANT: HOnjo, Tasuku
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: P1.178999
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
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SEQ ID NO 8
LENGTH: 198
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  US-09-966-880A-8
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-WODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_1/USPTPC_spool_1/TG0596680/runat_14062003_175526_10413/app_query.fasta_1.9493
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-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-buman40.cdi -LIST-45 -DCALIGEN-20 -HRE.SCORE-pct -THE_MAX-10
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-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-80 -THEADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Sequence 2, Appli
Sequence 174, App
Sequence 1639, Ap
                                                                                                                                                                     (without alignments)
6641.044 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PUS.PuB_UBDP:*
3: /cgn2_6/ptodata/1/pubpaa/PUSOB_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                       protein search, using frame_plus_n2p model
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US-09-966-880A-2
US-09-729-674-174
US-09-925-300-1639
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Sequence:

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Run on:

Scoring table:

Conservative: Mismatches: Length: Matches:

1.7e-94 1008.00 95.948 92.898

Indels: Gaps:

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JS-09-966-880A-2
                                                                   Percent Similarity:
Best Local Similarity:
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Matches:
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APPLICANT: HOLOGO, TASUKU
APPLICANT: MUTAMATION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-08801
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DYT/JP00/01918
PRIOR RILING DATE: 1090-00-28
PRIOR PILING DATE: 1999-12-77
PRIOR PILING DATE: 1999-12-77
PRIOR PILING DATE: 1999-12-77
PRIOR PILING DATE: 1999-12-77
PRIOR FILING DATE: 1999-12-77
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASLED for Windows Version 4.0
SEQ ID NO 2
LENGTH: 198
                                                     Gaps:
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Best Local Similarity:
Query Match:
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGA 591
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Steininger II, Robert J.
Spaulding, Vikki
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Treacy, Maurice
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AGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTC 312
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Patent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTYON: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: 2000-03-28
PRIOR FILING DATE: J000-03-28
PRIOR FILING DATE: J000-03-28
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     CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATENTIN Ver. 2.0
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369.50
58.52%
44.89%
33.56%
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Best Local Similarity:
Query Match:
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|HisAlaGluLeuCysPheLeuAspValIleProPheTrpLysLeuAspLeuAspGlnAsp
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
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83
31
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Matches:
Conservative:
Mismatches:
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
FRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 114
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Patent No. US20020151681A1
GENERAL INFORMATION:
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| Sequence 17. Application US/10073912
| Publication No. US20030077703A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT234C1
| CURRENT APPLICATION NUMBER: US/10/073,912
| CURRENT APPLICATION NUMBER: US/110/073,912
| Prior Application removed - See file Wrapper or Palm |
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 17
| LENTH: 18636
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Matches:
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Mismatches:
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PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PASKERQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 229
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CORGANISM: HOMO Sapiens
US-10-073-912-17
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                        20 ACCGGAGGAAGTTTCTTTACCAATTCA---AAAATGTCCGCTGGGCTAAGGGTCGGCGTG 76
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                                                                                   US-09-966-880A-7_COPY_80_676 (1-597) x US-10-073-912-17 (1-18636)
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Mismatches:
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Smith, Victoria
Watanabe, Colin K.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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1734 ThrGlyGlyAlaAlaAlaThrGlyAlaThrThrThrThrGlyAlaGly---GlyThrGly 1752
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   143 ATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTCTTCCTCCGCTACATCTCGGACT 202
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523 ThrCysThrGlyGlyGlyGlyCysAlaThrThrGlyThrAlaThrThrThrThrThr 542
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT PILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
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                                                    ACCTGTGCTACGTAGAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTT
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APPLICANT: Baker, Kevin P.
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Gurney, Austin L.
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Goddard, Audrey
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ORGANISM: Homo Sapien
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Best Local Similarity:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P343-8716217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT APPLICATION NUMBER: US/10/184,634
Prior Application removed - See File Wrapper or Palm
                                                                                   GGAGGAAGTTTCTTTACCAATTCAAAATGTCCGCTGGGCTAAGGGTCGGCGTGAGACCT
                                                                                                               432 GlyGlyGlyCysCysAlaGlyGlyCysAlaCysAlaGlyThrGlyGlyGlyCysAlaThr
                                                                                                                                                 83 ACCTGTGCTACGTAGTGAAGAGGCGTGACAGTGCTACATCCTTTTCACTGGACTTTGGTT
                                                                                                                                                                   505 ThrThrAla----ThrCysThrThrGlyCysThrGlyCysAlaThrGlyThrAlaThr
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                                                US-09-966-880A-7_COPY_80_676 (1-597) x US-10-184-644-303 (1-902)
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Matches:
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 Indels:
Gaps:
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Smith, Victoria
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US-10-184-634-303
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Best Local Similarity:
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LENGTH: 902
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1568 AlaglyCysCysThrGlyThrAlaThrTyrCysAlaThr---ThrThrGlyThrThrCys 1586
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TTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILNC DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                                                                                                                                                                                        Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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97.00
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US-10-184-634-319
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413 ThrThrThr-------ThrThrCysGlyAlaThrThrAlaAlaAlaGly 427
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 65
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                TCTTCACCGCGCCTCTACTTCTGTGAGGACCGCAAGGCTGAGCCCGAGGGGCTGC
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Matches:
Conservative:
Mismatches:
Indels:
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
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APPLICANT: Chen Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin
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US-10-184-634-65
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Best Local Similarity:
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Search completed: June 14, 2003, 19:09:17
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                               APPLICANT: Godowski, Paul J.
APPLICANT: Gorney Austin L.
APPLICANT: Gorney Austin L.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
APPLICANT: AND MODERED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184, 634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
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|1601 CysAlaGlyAlaAlaThrThrThrThrGlyAlaCys |||| |||
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Goddward, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Lang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-966-880A-7_COPY_80_676 (1-597) x US-10-184-634-319 (1-2103)
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35
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64
12
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Conservative:
Mismatches:
Indels:
Gaps:
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Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                               0.447
97.00
36.138
29.418
8.818
                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Homo Sapien
US-10-184-634-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                SEQ ID NO 319
LENGTH: 2103
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                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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1495 AlaThrCysAlaGlyGlyAlaAlaGlyThrAla------------ThrAla 1507
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| 1477 ThrGlyGlyAlaAlaCySGlyAlaGlyThrThrThrThrGly-----AlaGlyThrAla 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1508 ThrCysThrAlaThrAlaThrClyAlaThr-----CysThrThrClyAlaThrAlaThr 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 CCTGCTACGACTGTGCCCGACATGTGGCCGACTTTCTGCGAGGGAACCCCAACCTCAGTC
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|1584 CysGlyThrThrGlyGlyCysCysAlaCysGlyThrAlaGlyCys 1599
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P4430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
LENGTH: 1819
                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                       0.609
95.50
38.978
30.158
                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                     US-10-184-644-39
                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
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No..
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein June 14, 2003, 17:59:23; Search time 71 Seconds Run on:

(without alignments)
371.600 Million cell updates/sec

1086 1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 US-09-966-880A-8 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

A_Geneseq_101002:*

1. (SIDSZ/gcgdata/geneseqp/eenbl/AA1980.DAT:*
2. (SIDSZ/gcgdata/geneseqp/eenbl/AA1980.DAT:*
3. (SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
4. (SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
5. (SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
5. (SIDSZ/gcgdata/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		* Ouery				
NO.	Score	Match	re Match Length DB I	DB	ID	Description
1	1086	100.0	198	21		Human activation-i
2	1008			21	AAB24197	Mouse activation-i
e	390	35.9	384	20	AAY42383	Amino acid sequenc
4	390			22	AAU39075	Human secreted pro
'n	390			23	ABB55784	Human polypeptide
9	388			21	AAY84437	Amino acid sequenc
7	369.5			19	AAW77092	Human RNA editing
80	369.5			21	AAB11973	Human RNA editing
6	369.5			22	AAM38905	Human polypeptide
10	369.5			22	AAU23550	Novel human enzyme

polypep prostat human e RNA met Ruman e secreto	Human APOBEC2 prot A novel human mRNA Human polypeptide Novel human secret Novel human secret Human secreted pro Apo-B RNA editing Human protein segu	human secteted pro Drosophila melanog Peptide #5883 enco Protein #5554 enco Human brain expres Human bone marrow Peptide #5602 enco	Human transferase Pseudorables virus Human caspase-12 i Glycoprotein 50 (g Novel recombinant Pseudorables virus Pseudorables virus Pseudorables virus Human PRO-C-MG.72
AAM40691 AAB57061 AAU23537 AAE15256 AAB97879 ABB97879	AAE15900 AAW52131 AAO13149 AAO30166 AAG00666 AAR58705 AAR58704 AAR58704	AACU118b ABB62508 ABB38377 ABB3355 AAM58988 AAM11516 AAM11168 AAM11168 ABG41328 ABG41328	AAB73517 AAE05395 AAB16021 AAN76751 ABB78824 AAB78824 AAB7882501
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221 222 222 268 272 163	224 222 367 261 169 113 236 229	720 720 51 51 51 51 51 51 51 51 51	410 261 261 402 402 402 402 663
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369.5 369.5 369.5 336.5 309.5 309.5	274 262.5 208.5 204.5 203 199 198	03. 10. 88 88 88 88 91.	80.5 777.5 777.5 777.5
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ALIGNMENTS

AAB24198 standard; Protein; 198 AA (first entry) 05-FEB-2001 AAB24198; RESULT 1 AAB24198

Human activation-induced cytidine deaminase SEQ ID NO:8.

immune related disease; allergy; allergic disease; antiallergic; antianamenc; antiasthmatic; ophthalmological; anti-HIV; dermatclogical; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma: IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic collitis; duty allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; Activation-induced cytidine deaminase; AID; cytidine deaminase;

auto immunodeficiency syndrome; IgG subclass selection disorder

Homo sapiens.

WO200058480-A1 05-OCT-2000

2000WO-JP01918 28-MAR-2000; 99JP-0087192. 99JP-0178999. 99JP-0371382. 29-MAR-1999; 24-JUN-1999; 27-DEC-1999;

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05-0CT-2000
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The Draugh Structurally relates to an RNA editing enzyme APOBEC-1 and
has activity similar to APOBEC-1. AID has antiallergic,
constrained activities, and can be used in agene therapy. AID
dermatological activities, and can be used in gene therapy. AID
conversely activated activities and can be used in gene therapy. AID
treatment of B cell associated imments for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
timentodeficiency disease, ataxia telangiectasia, common variable
in deficiency disease, AIDS (auto immunodeficiency syndrome), elevated
in deficiency disease, AIDS (auto immunodeficiency syndrome), elevated
encoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for diagnosis and treatment of these disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy, allergic disease; antiallergic; antianament; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; Immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhintis; Rosen disease; bideorge disease; ataxia telanglectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease;
                                                                                                      Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVRRRDSATSFSLDFGYLRNKNGCHVELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse activation-induced cytidine deaminase SEQ ID NO:2.
                                                                                                                                                          Claim 1; Page 140-141; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB24197 standard; Protein; 198 AA.
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(NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                       Honjo T, Muramatsu M;
                                                               WPI; 2000-611715/58.
N-PSDB; AAC55312.
                                                                                                                                                                                                                                                                                                                                                                                                                 198 AA;
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The present sequence is mouse activation-induced cytidine deaminase
The Distructurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapy. AID
dermatological activities, and can be used in gene therapy. AID
polymoticatides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
disease, igh nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhintis, Rosen
colitis, asthma, food allergy, drug allergy, allergic rhintis, Rosen
immunodeficiency disease, ataxia telangiectasia, common variable
immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
indunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
indunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated
concoding AID may be used for gene therapy and the antibodies to the AID
protein may be used for diagnosis and treatment of these disorders.
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a target for drug development for immune-related diseases including
allergies -
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auto immunodeficiency syndrome; IgG subclass selection disorder.
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Pred. No. 6e-107;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 131-132; 174pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.88;
                                                                                                                                                                                                                                                                                                      99JP-0178999.
99JP-0371382.
                                                                                                                                                                                                                     28-MAR-2000; 2000WO-JP01918
                                                                                                                                                                                                                                                                               99JP-0087192
                                                                                                                                                                                                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC. (HONJ/) HONJO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Honjo T, Muramatsu M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-611715/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC55307
                                                                                                             WO200058480-A1.
                                                         Mus musculus.
                                                                                                                                                                                                                                                                            29-MAR-1999;
                                                                                                                                                                                                                                                                                                         24 - JUN - 1999;
27 - DEC - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY42383
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AAY42383
ID AAY4
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AC AAY4
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, sytemic lupus erythematosis, rheumatoid arthriis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by
116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                         Human; secreted protein; antiinflammatory; immunosuppressive; nouroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; periodontal disease; myeloid deficiency; wound healing; ulcer; periodontal disease; seteoporosis; osteoporathritis; Alzheimer's disease; parkinson's disease; Huttington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs K, McCoy JM, Lavallie E, Collins-racie LA,
Treacy M, Agostino MJ, Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 580-581; 619pp; English.
                                                                                                                                                                                                                                                                  AAU39075 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein lp547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2000; 2000US-0539330.
04-DEC-2000; 2000US-0729674.
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food supplement; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639363/73.
                                                                                             176 LRRIL 180
                                                                                                                                             375 LRAIL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS59293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H,
                                                                                                                                                                                                                                                                                                                AAU39075;
                                                                                                                                                                                                                    RESULT 4
                                             Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immulating (e.g. as vaccines) or suppressing activity, hemostatic hematopoiesis regulating activity, tissue growth activity, hemostatic activin/inhibin activity, chemoteatic/chemokinetic activity, activity, activity, neceptor/ligand activity, anti-inflammatory activity, activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting biorhythms or caricadic cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the 1p547\_4 protein, which is derived from the 1p547\_4 clone isolated from a human adult blood CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg
                                                                                                               secreted protein; cDNA library; clone; transmembrane protein; signal sequence cloning; hybridization cloning; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding human secreted proteins used for therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.9%; Score 390; DB 20; Length 384; 44.9%; Pred. No. 7.5e-36; ive 31; Mismatches 59; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agostino MJ, Steininger RJ;
                                                                                                                                                                                                                                                                                      278.290
/label= Leader/Signal peptide
291.384
/label= Mature protein
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                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                 Amino acid sequence of 1p547_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US03458.
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                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobs K, McCoy JM,
Treacy M, Aqostino M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-518580/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 AA;
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                                                                                                                                                                                                                    Homo sapiens
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17-FEB-1999;
                    09-DEC-1999
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                                                                                                                                                                  receptor.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; munue disorder: bacterial infection; fungal infection; cancer; tumour; autoimmune disorder: systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropethy; halpemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; neuroprotective; haemostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.
                                       infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration The protein, having activin or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility i female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention.
                                                                                                                                                                                                                                              6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC
                                                                                                                                                                                                                                                                                                                    Gaps
inflammatory processes, diseases of the peripheral nervous system, Alzheimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-brager syndrome, infections,
                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                            ; Score 390; DB 22;
; Pred. No. 7.5e-36;
31; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB55784 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 174.
                                                                                                                                                                                      35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9803-070346P
9803-070346P
9803-07055P
9803-071304P
9803-072134P
9803-072035P
9803-073035P
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                                                                                                                                                                                                                    83; Conservative
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             375 LRAIL 379
                                                                                                                                                            384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     LRRIL 180
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18-FEB-1998;
30-MAR-2000;
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                                                                                                                                                              Seguence
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The invention relates to isolated polynuclectides (ABA90876-ABA90968 and ABA90980) and encoded proteins (ABB55698-ABB5800), especially computated by the contained in polynuclectides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABB55707) contained in proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 care deposited with the American Type Culture Collection (ATCC) with accession number 98599. The polynuclectides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, cytostatic, anti-inflammatory activity and acting as cytokine modulators, and anti-inflammatory activity and acting as cytokine modulators, categories regulators, tissue growth modulators and/or cadherin therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial corting diseases: immune deficiency and disorders; e.g. bacterial corting diseases: incommune disorders, cancer, systemic lupus cythematosus or graft-versus-host disease; myeloid or lymphoid cell cythematosus or graft-versus-host disease; myeloid or lymphoid cell costeoarthritis; central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Partinson's disease, Huntington's costeoarthritis; central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Partinson's disease, Huntington's costeoarthritis; catend infarction or stroke; inflammatory sepsies or conjuncy, endotoxin lethality, arthritis, inflammatory bowel disease or companies. The disease or conjuncies or tumours or cancers, pemphigus vulgaris or pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFRAWECLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK------NGC 55
                                                                                                                                                                                                                                                                                                                                                                                                    New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations
                                                                                                                                                                                                                                                                                      Collins-Racie LA, Evans C;
Steininger RJ, Spaulding V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 384;
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44.9%; Pred. No. 7.5e-36;
11ve 31; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 311-312; 349pp; English.
                                                                                                                                                                                                                                                                                    , Lavallie ER,
M, Agostino MJ,
Fechtel K;
   98US-0197886.
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                                                                                        COLLINS-RACIE L
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                                                                                                                                          TREACY M.
AGOSTINO M J.
STEININGER R J
                                                                                                                                                                                             SPAULDING V.
WONG G G.
CLARK H.
                                                                                                                                                                                                                                                                                                    Treacy M,
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                                                                                                                                                                                                                                                                                    MCCOV JM,
                                                                                                                                                                                                                                                                                               J D, Tie.
                                                     MCCOY J M.
LAVALLIE E F
                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-040725/05
                                                                                                                         MERBERG D.
                                                                                                                                                                                                                                             (FECH/) FECHTEL K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 83; Conserv
                                        JACOBS K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABA90962
                                                                                                          EVANS
23-NOV-1998;
                                                                                                                                                                                                                                                                                    Jacobs K,
                                                                                                                                                                                                                                                                                                   Merberg D
Wong GG,
                                                                                      (COLL/)
(EVAN/)
                                 (JACO/)
(MCCO/)
(LAVA/)
                                                                                                                                                          (AGOS/)
(STEI/)
                                                                                                                                                                                           (SPAU/)
(WONG/)
(CLAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                         (MERB/)
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116 CEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, immune/inflammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, atherosclerosis, arteriosclerosis, myelofibrosis, paroxysomal nocturnal hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia and cancers, and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVELLFLRY ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK-----NGC
  a disorder associated with increased or decreased expression
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; RNA editing enzyme; REE; pharmaceutical carrier; cancer; viral disease; circulatory system disorder; RNA processing; hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                         Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                         35.7%; Score 388; DB 21;
44.3%; Pred. No. 1.3e-35;
ive 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human RNA editing enzyme protein sequence.
                                                             English.
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                                                             Claim 1; Page 101-102; 131pp;
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treating a disorder associa
of RNA associated proteins
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Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-505585/43.
N-PSDB; AAV48231.
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                                                                                                                                                                                                                                                                                                                                                     384 AA;
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                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                               Human: RNA-associated protein; cell proliferation; cancer; inflammation; immune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; arteriosclerosis; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis; trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and polynucleotides, useful for preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΰĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "potential phosphorylation site"
                                                                                                                                                                                                                                                                                     Amino acid sequence of a human RNA-associated protein.
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Lal P, Azimzai Y, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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98US-0158720.
98US-0186815.
99US-0128660.
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LRAIL 379
                     LRRIL 180
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04-NOV-1998;
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                   176
                                                           375
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                                                                                                                      RESULT
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Homo sapiens.
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                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                              The human RNA editing enzyme (REE) is used in a pharmaceutical carrier for the treatment of cancer, viral diseases and circulatory system tisocders. The enzyme is used in vivo for the correct processing of RNA transcripts of genes e.g. change of a codon in apolloporotein B (apoB) RNA to give a 100 and 48 kDa product transcribed from the same failure of apo B editing leads to excessive apoB 100 production and Finalure of apo B editing leads to excessive apoB 100 production and hypercholestrolaemia. Other disorders thought to be linked to incorrect RNA processing include aberrant alpha-galactosidase processing in recombinantly to treat related disorders. It can also be used to raise antibodies for immuno-based detection of REE expression levels
                                                                                                                                                                                                                                                                                                                                                    65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA editing enzyme; REE-2; human; HEPR homologue; REPR homologue; phorbolin I homologue; cancer; tumour; autoimmune disorder; circulatory system disorder: hypercholesterolaemia; viral infection; neurological disease; neurofibromatosis; transcript editing; detection.
                                                                                                                                                                                                                                                                                                    11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                            FYFQFKNLWBANDRNETWLCFTVEGIKRRSVVSWKT--GVFRNQVDSETHCHAERCFLSW
                                                                                                                                                                                                                                                                                                                                                                     125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex .
                                                                                                                                                                                                                                                            DB 19; Length 190;
                                                                                                                                                                                                                                                                                  64; Indels
disorders associated with incorrect RNA processing
                                                                                                                                                                                                                                                     34.0%; Score 369.5; DB 1
44.9%; Pred. No. 6.3e-34;
1ve 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB11973 standard; Protein; 190 AA.
                          Claim 1; Fig 1; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human RNA editing enzyme REE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0816241.
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                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                 Local Similarity
les 79; Conserv
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                                                                                                                                                                                                                             190 AA;
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                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                Best Loc
Matches
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This sequence represents the human RNA editing enzyme REE-2. CDNA encoding REE-2 was initially isolated in a prostate tumour cDNA library, with the cDNA encoding the present sequence representing a consensus. REE-2 has chemical and structural homology with the human apob mRNA cditing protein HEPR (28% identity), the rat HEPR homologue REPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity). REE-2 was found to be expressed in a variety of CDNA libraries, a high proportion of which were derived from tumours, neuronal CR EEE-2 is therefore thought to be associated with the development of cancer, autoimmune disorders, circulatory system disorders (e.g. cancer, autoimmune disorders, circulatory system disorders (e.g. chypercholesterolaemia), viral infections and neurological diseases (e.g. chypercholesterolaemia), wiral infections and neurological diseases (c.g. diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein crelates to methods of detecting nucleic acids man REE-2 in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%; Score 369.5; DB 21; Length 190; 44.9%; Pred. No. 6.3e-34; ive 24; Mismatches 64; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM38905 standard; Protein; 190 AA.
Claim 1; Fig 1A-B; 27pp; English.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AA;
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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2000US-0225758.
2000US-0225759.
2000US-022629.
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2000US-0217496.
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0000S-0227009.
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                        17-JAN-2001; 2001WO-US01239
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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  \times 5, 
                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous hocalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contraction activity, arthritis and inflammation, leukaemias and contractions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
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                                                                      Wang
                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                   Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.0%; Score 369.5; DB 22; Length 190; 44.9%; Pred. No. 6.3e-34; Live 24; Mismatches 64; Indels 9;
                                                                   Qian XB,
Yang Y,
                                                                 Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                  Example 3; SEQ ID NO 2050; 10078pp; English.
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Best Local Similarity 44.25.
Annual Similarity 44.25.
Annual Similarity 44.25.
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                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                        N-PSDB; AAI58061
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                                                                                                                 Zhao QA,
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Ruben SM;
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2000US-0241809.
2000US-0241826.
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2000US-0246619

2000US-0246611

2000US-0246611

2000US-0246611

2000US-0249208

2000US-0249212

2000US-0249213

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2000US-0237040.
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2000US-0249299.
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N-PSDB; AAS41420.
                                                   02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0C
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08-NOV-2000;
08-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000; 2
08-DEC-2000; 3
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders including hyperproliferative disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. athroids), cardiovascular disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. 65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. 11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64 preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's diseases, hamnostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation; 125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180 9; Gaps polypeptides and polynucleotides useful for diagnosing, 34.0%; Score 369.5; DB 22; Length 210; 44.9%; Pred. No. 7.3e-34; Live 24; Mismatches 64; Indels 9; Claim 11; SEQ ID No 1546; 1180pp; English. AAM40691 standard; Protein; 221 AA Human polypeptide SEQ ID NO 5622. 26-DEC-2000; 2000WO-US34263 21-JAN-2000; 2000US-0488725 22-OCT-2001 (first entry) Conservative Local Similarity nes 79; Conserv 210 AA; WO200153312-A1. Homo sapiens. 26-JUL-2001. diseases Sequence leukaemia. Query Match Best Local S AAM40691; Novel Matches RESULT 11 AAM40691 qq δ ò qq ò

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wound; infectious disease.
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                                                  WO200055174-A1
                            Homo sapiens.
                                                                                                    08-MAR-2000;
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Matches
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                                                                                                                                                                                                                                                                                            the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
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                                                                                                                                                                                                                                                                                                                                            system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotectic/chemokincic activity, amemostatic and thrombolytic activity, acceptance diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 FCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFQ-YPCYQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                             Wang
                                                                                                                                                                                                                   useful for treating disorders
                                                                                                                             Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.0%; Score 369.5; DB 22; Length 221; 44.9%; Pred. No. 7.8e-34; Ive 24; Mismatches 64; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer antigen protein sequence SEQ ID NO:1639.
                                                                                                                             Qian XB,
Yang Y,
                                                                                                                         Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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          09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0654191.
19-CCT-2000; 2000US-069336.
29-NOV-2000; 2000US-0727344.
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2000US-0552317
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nes 79; Conserv
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                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                      Zhou P,
                                                                                                                          Liu C,
Wang Z,
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                                                                                                                          Tang YT,
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proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.0%; Score 369.5; DB 2
44.9%; Pred. No. 7.9e-34;
:lve 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 2097-2098; 2338pp; English,
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                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
2000WO-US05988.
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nes 79; Conservative
                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
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21-SEP-200 25-SEP-200 25-SEP-200 26-SEP-200 27-SEP-200 29-SEP-200 29-SEP-200 29-SEP-200	R 29-SEP-2000; 2000US-0236370. R 02-OCT-2000; 2000US-0236370. R 02-OCT-2000; 2000US-0237039. R 02-OCT-2000; 2000US-0237039. R 02-OCT-2000; 2000US-0237039. R 13-OCT-2000; 2000US-023937. R 20-OCT-2000; 2000US-023937. R 20-OCT-2000; 2000US-0241286. R 20-OCT-2000; 2000US-0241808. R 20-OCT-2000; 2000US-024677. R 20-OCT-2000; 2000US-024672. R 08-NOV-2000; 2000US-024627. R 08-NOV-2000; 2000US-024621. R 08-NOV-2000; 2000US-024921. R 08-NOV-2000; 2000US	,
order; reproductive disorder; er; cytostatic; anti arthritic;	### ### ##############################	
inflammatory disorder; cardiovascular blood-related disorder; infectious disnephrotropic; anticoagulant. Homo sapiens. WO200155301-A2. 02-AUG-2001.	5 - 01790 5 - 01806 5 - 01806 5 - 01806 6 - 01806 6 - 01806 6 - 02186 6 - 02186	

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WO200183524-A2
                                                                              Homo sapiens.
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                                                                                                                                Peptide
                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of alsorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; RNA metabolism protein-19; RMEP-19; gout; nervous system disorder; autoimmune; inflammatory; cell proliferative; developmental; thyroiditis; gene therapy; epilepsy; dementia; stroke; Alzheimer's disease; amnesia; Parkinson's disease; prion disease; insomnia; endocrine disorder; AIDS; Acquired Immune Deficiency Syndrome; mental disorder; allergy; anaemia; asthma; atherosclerosis; Crohn's disease; rheumatoid arthritis; vaccine; glomerulonephritis; multiple sclerosis; diabetes mellitus; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                           preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 222;
                                                                                                                                                                                     Novel polypeptides and polynucleotides useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.0%; Score 369.5; DB 2
44.9%; Pred. No. 7.9e-34;
tive 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RNA metabolism protein-19 (RMEP-19).
                                                                                                                                                                                                                                                                                 SEQ ID No 1533; 1180pp; English.
                                                                                           Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE15256 standard; Protein; 268
                                                      (HUMA-) HUMAN GENOME SCI INC
11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 44.9%;
Conservative 2
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                                                                                           Barash SC,
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Best Local Similarity
                                                                                                                               WPI; 2001-465566/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AA;
                                                                                                                                                  N-PSDB; AAS41407
                                                                                                                                                                                                         preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                   Claim 11;
                                                                                           Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The invention relates to human RNA metabolism proteins (RMEP) and their corresponding cDNA molecules. RMEP and its DNA are used for diagnosing, treating and preventing nervous system disorders (epilepsy, dementla, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease); prion diseases; fatal familial insomnia, nutritional and metabolic diseases of the nervous system; inherited, metabolic, endocrine and coxic myopathy; mental disorders; dutoimmune/inflammatory disorders)

amnesia and Tourette's disorder; autoimmune/inflammatory disorders (AIDS-aquired immune deficiency syndrome, allergies, anaemia, asthma, gout, atherosclerosis, Crohn's disease, diabetes mellitus, glomerulonephritis, atheritis, osteoporosis, pancreatitis, systemic lupus sythematosus, clicerative colitis, and infections); cell proliferative disorders (cancer arteriosclerosis, cirrhosis, hepatitis, psoriasis); and developmental disorders (renal tubular acidosis). RMEP DNA is useful in drug screening techniques, gene therapy and for creating transgenic animals. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human RNA metabolism protein for diagnosing or treating nervous system disorders, autoimmune/inflammatory disorders, cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillman JL;
cancer; cirrhosis; hepatitis; psoriasis; transgenic animal; antiulcer; tranquilliser; drug screening; pancreatitis; renal tubular acidosis; systemic lupus erythematosus; colitis; ss.
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MG, Burford N, Batra S, Policky JJ;
                                                                                                                                                                                                                                                                                                                     22..268
/label= Mature_RMEP_19_protein
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                                                                                                                                                                                                                                                                                /label= Signal_peptide
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                                                                                                                                                                                                          Location/Qualifiers
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2000US-202090P.
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Baughn MR, Yao MG,
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nes 71; Conserv
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08-SEP-2000; 20 08-SEP-2000; 20 08-SEP-2000; 20 08-SEP-2000; 20 08-SEP-2000; 21 08-SEP-2000; 21 08-SEP-2000; 21 08-SEP-2000; 21 08-SEP-2000; 21 08-SEP-2000; 21 08-SEP-2000; 22 08-SEP-2000; 23 08-SEP-2000; 24 08-SEP-2000; 25 08-SEP-2000; 26 08-SEP-2000; 26 08-SEP-2000; 26 08-SEP-2000; 26 08-SEP-2000; 27 08-SEP-2000; 2
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17 - NOV - 2000;
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17-NOV-2000;
17-NOV-2000;
   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                               Novel human enzyme polypeptide #885
                                                   AAU23799 standard; Protein; 272
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20000S - 0.18664
20000S - 0.186464
20000S - 0.189874
20000S - 0.20515
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20000S - 0.215186
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20000S - 0.217886
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20000S - 0.22518
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2000US-0226279.
2000US-0226881.
2000US-0226868.
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18-MAR-2000; 29
18-MAR-2000; 20
27-JUN-2000; 20
28-JUN-2000; 20
17-JUL-2000; 21
11-JUL-2000; 21
11-JUL-2000; 21
11-JUL-2000; 21
14-MG-2000; 22
14-MG-2000; 23
14-MG-2000; 24
14-MG-2000; 25
14-MG-2000; 26
14-MG-2000; 
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24-FEB-2000;
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16-MAR-2000;
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                                                                                           AAU23799;
                    RESULT 15
                                      AAU23799
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The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                                                                                                                                  preventing, treating neural, immune system, muscular, reproductive, pulmomary, cardiovascular, renal, proliferative disorders and cancerous diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing,
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29.6%; Score 321.5; DB 22; Length
Best Local Similarity 45.3%; Pred. No. 3.2e-28;
Matches 68; Conservative 22; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVEN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 1795; 1180pp; English.
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                                            20000S-024930
20000S-0250160
20000S-025031
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2000US-0249299
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01 - DEC - 2000;
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Search completed: June 14, 2003, 18:09:11 Job time: 73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 14, 2003, 18:07:08; search time 41 Seconds (without alignments) 464.259 Million cell updates/sec Run on:

US-09-966-880A-8 1086 1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		apolipoprotein B m	apolipoprotein B m	В	В	М	hypothetical prote	hypothetical prote	fucosyltransferase	hypothetical prote			glycoprotein D pre	MacGAP protein [im	RW1 protein - mous	phosphogluconate d	hyaluronidase - ho	retinal pigment mi	conserved hypothet	mufl protein - hum	single-strand DNA-	UDP-galactose-lipi	site-specific reco	Hnr protein [impor		37K regulator resp	phosphogluconate d	1,4-alpha-glucan b	interferon precurs
		TD.	G01233	A53853	159323	JC4269	I48249	159577	S63464	T13412	C64601	S53921	T32318	T30999	VGBE50	659432	T14280	S15280	A47477	A47143	E70355	S52797	F97193	AC3455	S78538	A90846	н85703	A36871	DESHGC	AH0479	S57642
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æ	Query	Match	22.6		19.9	19.4	19.4	18.2	0.6	7.5	7.4	7.2	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.8	8.9	8.9	8.9	6.8	8.9	9.8	6.7
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Gaps

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Length 236;

Query Match 20.7%; Score 225; DB 2; Length 23 Best Local Similarity 37.4%; Pred. No. 6.8e-15; Matches 49; Conservative 26; Mismatches 48; Indels

0 1 1 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	72.5 72.5 72.7 72.7 72.7 72.7 71.5 71.5	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	446 1963 1963 312 443 3968 3968 3968 444 444 868	44444444444444444444444444444444444444	P71069 T019217 T019217 T01954 C84608 153035 143343 T23324 T43243 T23330 TVHUBD S10138 S10138	
4 4 3 C	71	9 0			SUBUBB TVHUDB	Ubb myeloperoxidase (E UDB transforming prote
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A;Cross C;Super Query Best Match	Cross-referer Superfamily: Query Match Best Local Si Matches 51;	rences: EMB y: apolipop h Similarity 51; Conser	ces: EMBL:U03891; apolipoprotein B 22.6%; milarity 46.4%; Conservative	103891; cein B 22.6%; 46.4%; ive	mRNA ed mRNA ed; Score; Pred.	EMBL:U03891; NID:g436940; PIDN:AAA03706.1; PID:g436941 .poprotein B mRNA editing enzyme, catalytic chain 1 22.6%; Score 245; DB 2; Length 116; 1ty 46.4%; Pred. No. 3.1e-17; servative 17; Mismatches 32; Indels 10; Gaps 3;
yo ga	76 Y 1 7 Y	YRVTWFT YRVTWFI	YRVTWFTSWSPCYD- YRVTWFISWSPCFSW	2 – 2 20 20 20 20 20 20 20 20 20 20 20 20 20	ARHVADFLI AGEVRAFL	RVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLH 130
oy da	131 F 62 D	RAGVQIA :: DAGAQVS	IMTEKDY: : :: IMTYDEF!	FYC. EYC!	ANTEVENH: : 	RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSYRLSROLRRIL 180 : :
RESULT 2 A53853 apolipoprotein B mRNA C;Species: Oryctolagu C;Date: 07-Oct-1994 C;Accession: A53853 R;Yamanaka, S.; Poksa J, Biol. Chem. 269, 2A;Title: Cloning and ributed. A;Reference number: AA;Accession: A53853 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-236 cYA A;Cross-references: G C;Superfamily: apolip C;Reywords: hydrolase	RESULT 2 A53853 apolipoprotein B mRNA editing enzyme, c.5pecies: Oryctologus cuniculus (don C.Date: 07-0ct-1994 #sequence_revisic C.Accession: A53853 R.Yamanaka, S.; Poksay, K.S.; Balestr J. Biol. Chem. 269, 21725-21734, 1994 A7:Title: Cloning and mutagenesis of tributed. A.Reference number: A53853 A.Accession: A53853 A.Accession: A53853 A.Stetus: preliminary A.Molecule type: mRNA A.Residues: 1-236 < YAM A.Cross references: GB:G10695; NID:g5 C.Superfamily: apolipoprotein B mRNA C.Keywords: hydrolase; zinc	tein B mRNA e Oryctolagus Oryctolagus Oct.1994 #sen n: A5383 , S.; Poksay, hem. 269, 217 hem. 269, 217 loning and mu e number: A53 preliminary type: mRNA : 1796: mRNA	A editing us cunicul #sequence_ay, K.S.; 21725-2173 I mutagenes A53853; MU AAA> GB:U10695; Epoprotein	9 e. ulu.e_r. . Be_r. 734 esi: MUII	n B mRNA editing enzyme, catalyt. yctolagus cuniculus (domestic ralyt.1994 #sequence_revision 07-Oct A53853 269. 21725-21734, 1994 269, 21725-21734, 1994 and mutagenesis of the rabbi. ing and mutagenesis of the rabbi. Iminary pe: mRNA -336 cYAM> ences: GB:U10695, NID:9506180; P: apolitoprotein B mRNA editing aydrolase; zinc	ESULT 2 53853 polipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4) - rabbit species: Oryctologus cuniculus (domestic rabbit) bate: O7-oct-1994 #sequence_revision 07-oct-1994 #text_change 18-Aug-2000 'Accession: A53853 Accession: A53853 'Yamanaka, S.; Poksay, K.S.; Balestra, M.E.; Zeng, G.Q.; Innerarity, T.L. Biol. Chem. 269, 21725-21734, 1994 Libuted. 'Ritle: Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A zinc motisputed. 'Reference number: A53853; MUID:94342367; PMID:8063816 'Scatus: preliminary 'Molecule type: mRNA 'Residues: 1-236 <yam> 'Cross-references: GB:U10695; NID:9506180; PIDN:AAA56718.1; PID:9506181 'Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1 'Keywords: hydrolass; zinc</yam>

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
C; Accession: 148249; 149287; 149286; 149288
C; Accession: 148249; 149287; 149286; 149288
R; Nakamuta, M.; Oka, K.; Krushkal, J.; Kobayashi, K.; Yamamoto, M.; Li, W.H.; Chan, L. J. Biol. Chem. 270, 13042-13056, 1995
A; Title: Alternative mRNA splicing and differential promoter utilization determine ti ion of Apobeci and related nucleoside/nucleotide deaminases.
A; Reference number: A57020; MUID:95286585; PMID:7768898
A; Retence number: A57020; MUID:95286585; PMID:7768898
A; Retus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-229 < RESS
A; Cross-references: EMBL:021951; NID:9899501; PIDN:AAC52211.1; PID:9899503
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-229 < RESS
A; Residues: 1-220 < RESS
A; Residues: 1-229 < RESS
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A;Accession: 149288
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C;Genetics:
A;Gene: MGI:Apobec1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
A;Reference number: JC4269; MUID:95408299; PMID:7677778
A;Accession: JC4269
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-229 <0SU>
C;Comment: This protein belongs to the cytidine deaminase gene family.
C;Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1
C;Keywords: hydrolase; zinc finger
F;48-96/Region: zinc finger HHCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 6/1; 15/2; 148/1; 187/3
C; Superfamily: apolipoprotein B mRNA editing enzyme, catalytic chain
C; Keywords: hydrolase
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Pred. No. 1.6e-13;
4; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 211; DB 2; 37.1%; Pred. No. 1.6e-13;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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A; Residues: 1-229 <RE4>
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Best Local Simi
Matches 49;
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C.Species: Homo saplens (man)
C.Species: Homo saplens (man)
C.Species: Homo saplens (man)
C.Date: 11-May-1966 #text_change 18-Aug-2000
C.Accession: 15923; 84253
R.Lau, P.P.; Zhu, H.J.; Baldini, A.; Charnsangavej, C.; Chan, L.
Proc. Nall. Acad. Sci. U.S.A. 91, 8825-8826, 1994
A.Title: Dimeric structure of a human apoll-poprotein B mRNA editing protein and cloning
A.Rccession: 15923; MUID:9435963; PMID:8078915
A.Accession: 15923; MUID:9435963; PMID:8078915
A.Accession: 15923; MUID:9435963; PMID:8078915
A.Rccession: 15923; MUID:9435963; PMID:8078915
A.Rccession: 15923; MUID:9435963; PMID:8078915
A.Rccession: 15923; MUID:9435963; PMID:8078915
A.Rccession: 15923; MUID:94268910; PMID:8078915
A.Rccession: 15923; MUID:94268910; PMID:826423
A.Rccession: 84523
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A.Rccession: 84523
A.Rccession: 84523
A.Rccession: 84523
A.Rccession: 159277; A4-226 CHAD>
A.Rccession: 159279; MIRD:94268910; PMID:8268612
A.Rccession: 159279; MIRD:94268910; PMID:826810;
A.Rccession: 159279; MIRD:94268910; PMID:826810;
A.Rccession: 159279; MIRD:94268910;
A.Rccession: 159279
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C; Species: Mus musculus (house mouse)
C; Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 18-Aug-2000
C; Accession: JC4269
R; Osuqa, J.; Inaba, T.; Harada, K.; Yagyu, H.; Shimada, M.; Yazaki, Y.; Yamada, N.; Biochem. Biophys. Res. Commun. 214, 653-662, 1995
A;Title: Cloning and structural analysis of the mouse apolipoprotein B mRNA editing
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                   RRETYLCYVVKRRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYRVTWF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4.-) - human
                                                                         RRDSATSFSLDFGYLR-----NKNGC-HVELLFL-RYISDWDLDPGRCYRVTWFTSWSP
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1 Similarity 34.9%; Pred. No. 4.8e-14;
44; Conservative 31; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                               142 KDYFYCWNTFV 152
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141 FKDYFYCWNTFV 152 :: 146 EQEYCYCWRNFV 157	DD 150 MNLRLSYLRDHTYPHLQVSVQSRDRVHNDGIEVLVVNYKFCRNTWNPFEIQFKMFYK 206 Qy 154 NHERTFKAWEGLH-ENSVRLSRQLRRILLPLYEVDDLR 190
RESULT 6 159577 apolipoprotein B mRNA editing enzyme, catalytic chain 1 (EC 3.5.4) - rat	Db 207 FEDSTLLKWEILRISTNVRLKAKQLLATRNPQKCLLSLYEFDKIK 251 RESULT 8
ies: Rattus norvegicus (Norway rat.) : 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000 ssion: I59577 : B.; Burant, C.F.; Davidson, N.O.	T13412 hypothetical protein 133E12.4 - fruit fly (Drosophila melanogaster) Species: Drosophila melanogaster C; Species: 13.Aug-1999 #sequence_revision 13.Aug-1999 #text_change 17.Nov-2000
Aritie: Molecular cloning of an apolipoprotein B messenger RNA editing protein. A.Title: Molecular cloning of an apolipoprotein B messenger RNA editing protein. A.Reference number: I59577; MUID:93289362; PMID:8511591 A.Accession: I59577 A.Stetus: prediminary; translated from GB/EMBL/DDBJ	Cyaccession: 11341. Cyaccession: 11341. Rymrphy, L.; Harris, D.; Barrell, B. Submitted to the EMBL Data Library, April 1999 A; Description: Sequencing the distal X chromosome of Drosophila melanogaster. A; Reference number: 217668
dues: 1-7pc: mins dues: 1-2pc: RESA 18-references: GB:L07114; NID:g467808; PIDN:AAA17394.1; PID:g347165 srfamily: apolipoprotein B mRNA editing enzyme, catalytic chain 1 ords: hydrolase	Afforcession: 113412 A;Molecule type: DNA A;Residues: 1-2342 <mur> A;Cross-references: EMBL:AL009192; NID:e1371524; PID:e1202150; PIDN:CAA15686:1</mur>
Query Match 18.2%; Score 198; DB 2; Length 229; Best Local Similarity 32.9%; Pred. No. 3.3e-12; Matches 56; Conservative 24; Mismatches 62; Indels 28; Gaps 6;	C;Genetics: A;Cross-references: FlyBase:FBgn0000667 A;Introns: 1161/3; 1205/1; 1283/1; 1432/3; 1489/2; 1912/3 A;Note: EG:133E12.4
24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGR 74 1 1 1 1 1 1 1 1 1	Query Match 7.5%; Score 81.5; DB 2; Length 2342; Best Local Similarity 25.5%; Pred. No. 19; Matches 25; Conservative 15; Mismatches 29; Indels 29; Gaps 3;
75 CYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGV 134 : : : ::	QY 94 VADFLRGNPNLSLR-IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKD 143 :::
135 QIAIMTEKDYEYCWNTEVENHERTFKAWEGLHENSVRLSRQLRRILLPLY 184 	Qy 144 YFYCWNTFVENHERTFKAMEGLHENSVRLSRQLRRILL 181 1
RESULT 7 S63464 hypothetical protein YPL018w - yeast (Saccharomyces cerevisiae) N:Alternate names: hypothetical protein LPB13w C:Species: Saccharomyces cerevisiae C:Species: S63464 A:Bondecule to the EMBL Data Library, September 1995 A:Rocession: S63464	RESULT 9 C64601 fucosyltransferase - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 C;Accession: C64601 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mqtk son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Accession: C64601 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Mosleule type: DMA A;Residues: 1-476 <-TOM>A;Residues: 1-476 <-TOM>A;Residues: 1-476 <-TOM>A;Cross-references: GB:AE000578; GB:AE000511; NID:92313759; PIDN:AAD07710.1; PID:923
Query Match 9.0%; Score 97.5; DB 2; Length 369; Best Local Similarity 22.2%; Pred. No. 0.06; Matches 50; Conservative 34; Mismatches 70; Indels 71; Gaps 11;	Ouery Match 7.4%; Score 80; DB 2; Length 476; Best Local Similarity 20.8%; Pred. No. 4.5; Matches 43; Conservative 21; Mismatches 57; Indels 86; Gaps 10;
2 DSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL- 60 1:1	QY 7 NRRKFLYQFKNVRWAKGRRETYLCYVVRRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66 1:: : : : : : : :
61FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPN 103	Qy 67 DALDPGRCYRVIWFISWSPCYDCARHVADFLRGNPNLSLR 107

	C; Accession: T32318 R; Blanchard, M.; Kramer, J; Elliott, G.; Twyman, B. S; Blanchard, M.; Kramer, J; Elliott, G.; Twyman, B. A; Description: The EMBL Data Library, September 1997 A; Rectence number: 221149 A; Accession: T33318 A; Concelle type: DNA A; Residues: 1-251 CBLA> A; Residues: 1-251 CBLA> A; Residues: 1-251 CBLA> A; Genetics: A; Map posttion: 5 A; Amp posttion: 5 A; Introns: 53/2 C; Superfamily: Caenorhabditis elegans hypothetical protein K06B4.9 Cuery Match Best Local Similarity 26.8%; Pred. No. 3.9; A; Introns: 53/2 C; Superfamily: Caenorhabditis elegans hypothetical protein K06B4.9 Cuery Match Best Local Similarity 26.8%; Pred. No. 3.9; A; Introns: 53/2 C; Superfamily: Caenorhabditis elegans hypothetical protein K06B4.9 Cuery Match Best Local Similarity 26.8%; Pred. No. 3.9; Autches 40; Conservative 13; Mismatches 51; Indels 45; Gaps 7; Db 78 MLSLLMALNRFRAVFWYLRYNRIFFWRNFGCLVFAVIYILYD 126 Cy 52 KNGCHVELLELRYISDMDLDPGRCTRYTHFTSWSPCYDCARHVAPFIND 126 Cy 52 KNGCHVELLELRYISDMDLOFGRCTRYTHFTSWSPCYDCARHVAPFIND 126 Cy 52 KNGCHVELLELRYISDMDLOFGRCTRYTHFTSWSPCYDCARHVAPFIND 126 Cy 52 KNGCHVELLELRY	RESULT 12 T30999 PT30999 PT30999 PT30999 PT30999 C: Secretary protein F5686.5 - Caenorhabditis elegans C: Date: 22-Oct-1999 #text_change i7-Mar-2000 C: Cacession: T30999 R: Stellyes, L.; Stellye, L. R: Stellyes, L. R: St
Qy 108 IFTARLYFCEDRRAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWE 163 1	Apr-2002 9791130 onzalez, rm of Sac rm of Sac 7791130 ary, Nove	C. C.

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C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C. Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C. Accession: T14280
C. Milkinson, R.; Fitter, S.; Tscharke, D.; Simmons, A.
Submitted to the EMBL Data Library, April 1998
A; Reference number: 217958
A; Reference number: 217958
A; Reference number: 217958
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Residues: 1-1829 < WIL>
A; Cross-references: EMBL. AF060565; NID:q3091277; PID:q3091278; PIDN:AACI5232.1
A; Experimental source: strain BALB/c; brain
                                                                                                                            69 DLDPGRCYRVT--WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||:
|--KSEPK-- 715
                                                                                                132 AGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGL--HENSVRLSRQLRRILLPLYEVDDL 189
  73 GRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL-RIFTARLYFCEDRKAEPEGLRRLHR 131
                                                264 OKAVKIKTKDSGLFCVPLTALLEQDORKVPGMRIPLIFOKLISRIEERGLETEGLLRIPG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 -----VQPGVAMQED---LWNADWDAHQSLFKAWMGIKENA 748
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40;
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27.2%; Pred. No. 40;
tive 15; Mismatches
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376 K-AFQAV 381
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 02-Aug-2002
C;Accession: 659432
R;Uchida, T.; Kuramasu, A.; Okumura, K.; Nakao, A.; Ogawa, H.; Ra, C.
Submitted to GenBank, December 2001
A;Referrence number: 659432
A;Accession: 659432
                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: A27788
R;Petrovskis, E.A.; Timmins, J.G.; Armentrout, M.A.; Marchioli, C.C.; Yancey Jr., R.J.; J. Virol. 59, 216-223, 1986
A;Title: DNA sequence of the gene for pseudorables virus gp50, a glycoprotein without N-A;Reference number: A27788; MUID:86281819; PMID:3016293
A;Accession: A27788
A;Accession: A27788
A;Residues: 1-402 <PET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                            ---FCKLREA-AKGSRRLHRNKRSRSSYQRVTRSVQRVVLF--- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIA-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 TPMWWTPSADYMFPTEDEL------GLLMVAPGRFNEGOYRRLVSVDGVNILTD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISDWDLDP----GRCYRVT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 KNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISD---WDLDP 72
                                                                                                                                                                                                                                                                                                                                       C:Species: suid herpesvirus 1
A:Note: host Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: GB:M14001; NID:g334051; PIDN:AAC35203.1; PID:g334052 C; Superfamily: herpesvirus glycoprotein D C; Superfamily: herpesvirus glycoprotein by Coprodes: glycoprotein; transmembrane protein F:1-17/Domain: signal sequence #status predicted <SIG> F:18-402/Product: glycoprotein D #status predicted <GPD> F:362-378/Domain: transmembrane #status predicted <IMN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Residues: 1-618 <UCH>
A:Cross-references: GB:NP_277050; PID:g15723376; PIDN:NP_277050.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73; Indels
                                             144 YFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILLPL----
                                                                                                                                                                                                                                                                                                                 glycoprotein D precursor - suid herpesvirus 1 (strain Rice)
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Best Local Similarity 24.9%; Pred. No. 6.6;
Matches 42; Conservative 17; Mismatches
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ENFRTAFKSL 279
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42; Conserv
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A;Molecule type: mRNA
A;Residues: 1-618 <UCH>
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Best Local S
Matches 42
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 14, 2003, 17:59:53 ; Search time 24 Seconds (without alignments) 342.180 Million cell updates/sec Run on:

US-09-966-880A-8 1086 1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Length	DB :	QI	Description
7	364	33.5	382	Н	PHB3_HUMAN	
7	363.5	33.5	199	-4	PHB1_HUMAN	homo
٣	339	ᆸ	190	, -	PHB2_HUMAN	homo
4	225	20.7	236	-	ABME_RABIT	
S	216.5	19.9	236	-	ABME_HUMAN	
9	211	19.4	229		ABME_MOUSE	-
7	198	18.2	229	-	ABME_RAT	P38483 rattus norv
80	97.5	•	369	Н	CT19_YEAST	Q02732 saccharomyc
6	85	٠	503	7	MATK_KUNBA	Q9tkc0 kunzea baxt
10	78.5	7.2	817	-	YG4B_YEAST	P46951 saccharomyc
11	77.5	7.1	402	٦	VGLD_PRVRI	P07645 pseudorabie
12	77	7.1	1829	٦	RW1_MOUSE	070472 mus musculu
13	75.5	٠	382	٦	HUGA_APIME	Q08169 apis mellif
14	75	•	354	Н	WN14_CHICK	
15	m	•	337	-	HNR_ECOLI	
16	73.5		482	Н	6PGD_SHEEP	P00349 ovis aries
17	ω.		738	Н	TRFM_MOUSE	Q9r0r1 mus musculu
18	ς.	6.7	191	-	INF_ANAPL	P51526 anas platyr
19	ď		641	Н	PAPB_MOUSE	Q9wvp6 mus musculu
20	72		357	7	WN15_HUMAN	_
21	72	•	433	7	ERF1_SCHPO	P79063 schizosacch
22	72		792		GUAA_CAEEL	Q09580 caenorhabdi
23	72		811	Н	SYM_TREPA	083776 treponema p
24	72		1094	-	DPOL_GPCMV	_
25	72		3866	Н	HRX_MOUSE	_
26	7		3969	Н	HRX_HUMAN	Q03164 homo sapien
27	71.5		505	Н	FIXL_BRAJA	P23222 bradyrhizob
28	71		330	-	PHTD_COMTE	Q59727 comamonas t
29	7.1	•	718	-	PERM_MOUSE	mus m
30	71		925	-	DBL_HUMAN	homo
31	\sim	6.5	1805	-	RW1_HUMAN	homo sa
32	70.5	6.5	630	H	FIMB_CHICK	gallu
33	70	6.4	626		HCY6_ANDAU	androct

P10844 clostridium P75919 escherichia	Q9nrj5 homo sapien Q929h0 pseudomonas	P57528 buchnera ap	P29416 mus musculu	Q9163/ xenopus lae	Polobo escherichia	Place red clover	P29837 l genome po	P11935 c cephalosp	P55615 rhizobium s
BXB_CLOBO YMDC ECOLI	PAPB_HUMAN GLND_PSEAE	EX5C_BUCAI	HEXA_MOUSE	KIFZ_XENLA	TNP9_ECOL1	VGNM_RCMV	POLG_LANVT	EXPA_CEPAC	Y4PF_RHISN
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34	36	38	36	0 .	41	47	43	44	45

ALIGNMENTS

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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration the European the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 LYFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of phorbolin 3.";
Submitted (JUN-1996) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEDXXCYTIDINIATE DEAMINASES
FAMILY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-148 IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                      5 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Epidermis;
MEDLINE-99399284; PubMed-10469298;
Madsen P.P., Anant S., Rasmussen H.H., Gromov P., Vorum H.,
Dumanski J.P., Tommerup N., Collins J.E., Wright C.L., Dunham I.,
Macginnitie A.J., Davidson N.O., Cells J.E.;
"Psoriasis up-regulated phorbolin-1 shares structural but not functional similarity to the mRNA-editing protein apobec-1.";
J. Invest. Dermatol. 113:162-169(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                                            382 AA; 45924 MW; DA6EDD23E8856240 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     33.5%; Score 364; DB 1;
43.5%; Pred. No. 2.5e-29;
ilve 26; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731941; 012807;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
              human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 AA
                                                                                                                                                                                                                                                                                                       InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                               EMBL; AL022318; CAB45270.1; -.
                                                SEQUENCE OF 148-382 FROM N.A.
                                                                                                                                                                                                                                                                                           U61084; AAD00090.1;
                         Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 43.5
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 VRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || :|| ||
367 QALSGRLRAIL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
Tilahun Y., Wright H.;
                                                            TISSUE-Keratinocytes;
                of
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                                                                                                                                                     INITIATOR
                                                                                                                                                                                                                                                                                                                               Hydrolase.
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                                                                           Madsen P.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Best Local 9
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PHB1_HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LMDPHIFTSNFNN---GIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLLCGFYG 68
                                                                                                                                                                                     DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of phorbolin 2.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE CYTIDINE AND DECXYCYTIDYLATE DEAMINASES
FAMILY: STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----G
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                 "Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).

-: SIMILARITY: BELONGS TO THE CYTIDINE AND DECXYCYTIDYLATE DEAM FAMILY STRONG, TO APOLIPOPROTEIN B MRNA EDITING PROTEIN.
                                                            Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.
Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 AA; 23012 MW; 42E99E0D7DF7AA14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 363.5; DB 1
43.5%; Pred, No. 1.3e-29;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           112-121 AND 129-137
                  TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
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16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Q9UE74;
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us-09-966-880a-8.rsp

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Davidson N.O.
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P41238;
 METAL
METAL
METAL
DOMAIN
MUTAGEN
MUTAGEN
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   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                           HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARL 113
                                                                                                                                                                                                                                                                                                                                       114 YFCEDRKAEP---EGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSV 170
                                                                                                                                                                                                                                                                                                                                                          HADWRFLDLVPSLQLDPAQIYRVTWFISWSPCFSWGCAGEVRAFLQENTHVRLPIFAARI 120
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-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND MUTAGENESIS.
STRAIN-New Zealand white; TISSUE-Small intestine;
MEDLINE-94342567; Pubmed-8063816;
Wamanaka S., Poksay K.S., Balestra M.E., Zeng G.-Q., Innerarity T.L.;
"Cloning and mutagenesis of the rabbit ApoB mRNA editing protein. A
zinc motif is essential for catalytic activity, and noncatalytic
auxiliary factor(s) of the editing complex are widely distributed.";
J. Biol. Chem. 269:21725-21734(1994).
-I- FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF
A.C.A. CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
                                                                                                                                                                                                           6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRN--KN-----GC
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                             20;
                                                                                                                                               Length 190;
                                                                                                                                                                            65; Indels
                                                                                                            190 AA; 22453 MW; A54DCBC100FC26F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-FEB-1996 (Rel. 33, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
                                                             InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; FALSE_NEG
                                                                                                                                            31.2%; Score 339; DB 1;
41.1%; Pred. No. 3.7e-27;
tive 27; Mismatches 65;
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InterPro; IPR002125; dCMP/cyt_deam.
Pfam; PF003183; dCMP_cyt_deam; 1.
PR051TE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
entities requires a license agreement (or send an email to license@lisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                           EMBL; U61083; AAD00089.1;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       171 RLSRQLRRIL 180
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                                                                                                                                                           Local Similarity
nes 78; Conserv
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                                                                                             Hydrolase.
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                                                                                                          SEQUENCE
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Matches
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-i- CORCACTOR: ZINC (BY SIMILARITY).
-i- SUBUNT: HOMODIMER.
-i- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE.
-i- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYRVTWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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TISSUB-small intestine;
MEDLINE-94359963; PubMed-8078915;
Lau P.P., Zhu H.-J., Baldini A., Charnsangavej C., Chan L.;
"Dimeric structure of a human apolipoprotein B mRNA editing protein and cloning and chromosomal localization of its gene.";
proc. Natl. Acad. Sci. US.A. 91:8522-8526(1994).
                                                                                                                          H->A: NONE OR LITTLE EDITING ACTIVITY.
H->C: RETAINS MOST EDITING ACTIVITY.
E->A: NONE OR LITTLE EDITING ACTIVITY.
P->A: RETAINS MOST EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
C->A: NONE OR LITTLE EDITING ACTIVITY.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujino T., Navaratnam N., Scott J.;
"Human apolipoprotein B RNA editing deaminase gene (APOBECI).";
Genomics 47:266-275(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
8
                                                                                                                                                                                                                                                                                                                                                                                           Score 225; DB 1; Length 236; Pred. No. 1.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hadjiagapiou C., Giannoni F., Funahashi T., Skarosi S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (HEPR).
                                                                                                                                                                                                                                                                                                                           27719 MW; AB3041CA5102F1F3 CRC64;
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
H->A: NONE OF LITTLE ED
H->C: RETAINS MOST EDITE
E->A: NONE OR LITTLE ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Score 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Peripheral blood leukocytes;
MEDLINE-98140126; PubMed-9479499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Intestine;
MEDLINE=94268910; PubMed=8208612;
                                                                                                                                                                                                                                                                                                                                                                                               20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 KDYFYCWNTFV 152
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                              236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKEACLLYEIKWGMSRKIWRSSGKNTTNHVEVNFIKKFTSERDFHPSISCSITWFLSWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamuta M., Oka K., Krushkal J., Kobayashi K., Yamamoto M., Li W.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alternative mRNA splicing and differential promoter utilization determine tissue-specific expression of the apolipoprotein B mRNA-editing protein (Apobecl) gene in mice. Structure and evolution of Apobecl and related nucleoside/nucleotide deaminases."; J. Biol. Chem. 270:13042-13056(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42866DEF9FD1A877 CRC64;
                                                                                                                                                                                                                                                                                                                                        ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
S -> T (IN REF. 1).
S -> T (IN REF. 1).
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16-0CT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1).
APOBECI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AA
                                                                                                                                                                                                                                                                                 Pfam; Processing, dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                            EMBL; AB009426; BAA23882.1; -. EMBL; AB009422; BAA23882.1; JOINED. EMBL; AB009423; BAA23882.1; JOINED. EMBL; AB009424; BAA23882.1; JOINED. EMBL; AB009425; BAA23882.1; JOINED. PIR; S45253; S45253.
                                                                                                                                                                                                                                                                                nterPro; IPR002125; dCMP/cyt_deam.
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MEDLINE-95286585; PubMed-7768898;
                                                                                                                                                                                                                                                                                                                                         61 61 21
93 93 22
96 95 21
180 193 LE
83 83 83
236 AA; 28173 MW;
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                                                                                                                                  EMBL; L25877; AAA86766.1; -.
                                                                                                                                                                                                                                                  Genew; HGNC:604; APOBEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 CWNTFV 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                MIM; 600130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABME_MOUSE
P51908;
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DOMAIN
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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                                                                                    -!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 RRETYLCYVVK -- RRDSATSFSLDFGYLRNKNGCHVELLFL-RYISDWDLDPGRCYRVTW
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
A CAA CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA.
-!- COFFACTOR: ZINC (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY ZIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teng B., Burant C.F., Davidson N.O.; "Molecular cloning of an apolipoprotein B messenger RNA editing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 211; DB 1; Length 229; 37.1%; Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Apolipoprotein B mRNA editing protein (APOBEC-1) (REPR).
APOBEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
LEU-RICH MOTIF.
W; 1CBCF9929066ABAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Spraque-Dawley; TISSUE-Small intestine; STRAIN-S2289362; PubMed-8511591; Teng B., Burant C.F., Davidson N.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00383; dCMP_cyt_deam; 1.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                      EMBL, U21951; AAC52211.1; --
EMBL, U21947; AAC52211.1; JOINED.
EMBL, U21949; AAC52211.1; JOINED.
EMBL, U21950; AAC52211.1; JOINED.
EMBL, U2262; AAC52211.1; JOINED.
EMBL, U2262; AAC5221.1; --
EMBL, U2264; AAC5221.1; --
EMBL, U2264; AAC5221.1; --
MGD, MGI:103298; APOPECI.
InterPro; IPR002125; GCMP/cyt_deam.
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01-OCT-1994 (Rel. 30, Last seq
16-OCT-2001 (Rel. 40, Last anno
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27521 MW;
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146 EQEYCYCWRNFV 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 49; Conserv
                                                                      INTESTINE
                                                                                                        FAMILY
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S0005939; CTF19.
ENCE 369 AA; 4
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Best Local
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MEDLINE-9731371; PubMed-9169875;
MEDLINE-9731371; PubMed-9169875;
MEDLINE-9731371; PubMed-9169875;
MEDLINE-9731371; PubMed-9169875;
MEDLINE-9731371; PubMed A., Albermann K., Allen E., Ansorge W Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
Dietrich F.S., Delius H., Dibaolo T., Dabois E., Duesterhoeft A.,
Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
                       CODON FOR GLN TO A UAA CODON FOR STOP IN THE APOB MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                          COFACTOR: ZINC (BY SIMILARITY).
SUBUNIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE LIVER AS WELL AS SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 QIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILLPLY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TIQIMTEQESGYCWRNFVNYSPSNEAHWPRYPHLWVRL-----YVLELY 183
  FUNCTION: RESPONSIBLE FOR THE POSTRANSCRIPTIONAL EDITING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.2%; Score 198; DB 1; Length 229; 32.9%; Pred. No. 7.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyland K.M., Hieter P.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08766441882789B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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15-JUN-2002 (Rel. 41, Last annotation update)
Kinetochore protein CTF19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEU-RICH MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002125; dCMF/cyt_deam.
Para; FP00083; dCMP_cyt_deam; 1.
PR0STTE: PS00903; CYT_DCMP_DEAMINASES; 1.
mRNA processing; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27274 MW;
                                                                                                                                                                                                                                                                                                                                                                               EMBL; L07114; AAA17394.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                              INTESTINE
                                                                                                                                                          FAMILY.
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002732;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----FLRYISDWDLDPG-----RCYRVTWFTSWS----PCYDCARHVADFLRGNPN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 NDITQDFLNLISISSSNPNSAISDRKRVERINGLTNLQKELVTKYDTLPLL-----N 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNT-----FVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 MNLRLSYLRDHTYPHLQVSVQSRDRVHNDGIEVLVVNYK---FCRNTMNPFEIQFKMFYK 206
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                                                                                                                                                                                                                                                                                                                                                          "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 DALLTRRNTLLQEI------QTYQNILMKENNSKT------KNG---DILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Myrtales; Myrtaceae; Kunzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messequy F., Mawes H.-w., Mirtipati S., Moestl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scharens B., Schramm S., Schroder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 97.5; DB 1; Length 369; 22.2%; Pred. No. 0.018; Live 34; Mismatches 70; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 NHERTFKAWEGLH-ENSVRL-----SRQLRRILLPLYEVDDLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 FEDSTLLKWEILRISTNVRLKAKQLLATRNFQKCLLSLYEFDKIK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42782 MW; 23B4CBD6AE26E793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION: IMPORTANT FOR CHROMOSOME SEGREGATION.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U72265; AAB17275.1; -. EMBL; U36624; AAB68169.1; -.
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Pred.

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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                    112 FSLERKEIAKSYNLRSIHSIFSFLEDKFTHLDYVSDVLIPYHIHLEILXQTLKY---WVK 168
                                                                                                                                                                                                                                                                                                                               71 DPGRCYRVTWFTS--WSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRR 128
                                                                                                                                                                                                                                                                                                                                                  ----NGCHVELLF--LRYISDWDL
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces cerevisiae chromosome VII contains four previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YG4B_YEAST STANDARD; PRT; 817 AA.
P46951;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOThetical 95.4 kDa protein in SNGI-PMT6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guerreiro P., Maia e Silva A., Barreiros T., Arroyo J., accia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada C.,
                                                                                                                                                                                                                      7.8%; Score 85; DB 1; Length 503;
                                                                                                                                                                                                                                                       52; Indels
                                                                                                                                                                                              B114A4704FCEA059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95365 MW; AC42730C8B9C3E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                       Pred. No. 0.47;
                                                                                                                                                                                                                                 25.0%; Pred. ...
                                                                                                                         InterPro; IPR000442; Intron_maturse2. InterPro; IPR002866; Matk_N. Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; Matk_N. 1. Chloroplast; mRNA processing. SEQUENCE 503 AA; 60203 MW; B114A47
                                                                                                                                                                                                                                                                           31 YVVKRRDSATSFSLD-----FGYLRNK-
                                                                                                                                                                                                                                                                                                                                                                                     129 -- LHRAGVQIAIMTFKDYFY 146
                                                                                                                                                                                                                                                                                                                                                                                                         226 QSSHLRSTSSGIFXERIYFY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96076633; PubMed-7502584;
                                                                                                            EMBL; AF184722; AAF05929.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown open reading frames.";
Yeast 11:1087-1091(1995).
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.0°
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S0003430; YGR198W.
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817 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4932;
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SEQUENCE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Length 817;

DB 1;

7.2%; Score 78.5;

Query Match

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6
                                                                             41 SFSLDFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRG 100
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                                                                                                                        ----VYPGNISKVL-TNAWSTLYEIRKYOLDFLVS 455
                                                                                                                                                                 101 NPNLSLRIFTARLYFCEDRK------AEPEGLRRL------HRAGVQIAIMTF 141
                                                                                                                                                                                                                                                   142 K------DYFYCWNTFV-----ENHERTFKAW------EGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                 88 RRPTYRAHV------AWYRIADGCAHLLYFIEYA---DCDPROVFGRCRRRT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIA-- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 TPMWWTPSADYMFPTEDEL------GLLMVAPGRFNEGQYRLVSVDGVNILTD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 RRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISDWDLDP----GRCYRVT 79
                                                                                                                                                                                                        N-NLTSYLCNAMMLSTKEKDNADVEEQEEGEEEKALRELQFKYSYTLAQQRHIETAIKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 402;
                                             Indels
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17; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 AA; 44501 MW; B8763305995871E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein GB50.
Pseudorabies virus (strain Rice) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
NCBL_TaxID=10350;
                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                      ed. No. 3.7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 77.5;
24.9%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR002896; Herpes_glycop_D.
Pfam; PF01537; Herpes_glycop_D; 1.
21.3%; Pre-
                                                                                                                        413 SESLD--WLENSTRC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:-
                                                                                                                                                                                                                                                                                                                                        180 LLPLYEVDDLRDAFRTL 196
                                                                                                                                                                                                                                                                                                                                                                   | | | :: : | ||
575 HLKLTQLALIEEIFGTL 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M14001; AAC35203.1; -. PIR; A27788; VGBE50.
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGLD_PRVRI
                                                                                                                                                                                                             456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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141 FK-----
                                                                                                                                                                                                hyaluronate.
  TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
WN14_CHICK
                                                                                                                                          e 1.";
Anal.
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Matches
  HIAU
HIAU
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                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLDPGRCYRVT - - WFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---KSEPK-- 715
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Allergen Api m 2) (Api m II).
Apis mellifera (Honeybee).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Bee venom hyaluronidase is homologous to a membrane protein of
179 FMVALPEGQECPFARVDQH-RTYKFGACWSDDSFKRGVDVMRFLTPFYQ 226
                                                                                                                                                                                                        STRAIN-BALB/c; TISSUE-Brain; Wilkinson R.; Fitter S., Tscharke D., Simmons A.; Wilkinson R., Eutter S., Tscharke D., Simmons A.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 77; DB 1; Length 1829; 27.2%; Pred. No. 13; Live 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 DLEPGKKSKIANIYFDPGLQCGD-HRYI----GLPFLS-----
                                                                                                                                                                                                                                                                                                                                                                                   927110; RW1.
1829 AA; 200508 MW; D0B3E209257AFAE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammalian sperm.";
Proc. Natl. Acad. Sci. U.S.A. 90:3569-3573(1993).
                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥
                                                         A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Venom gland;
MEDLINE-93234539; PubMed-7682712;
Gmachl M., Kreil G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aculeata; Apoidea; Apidae; Apis
                                                                             (Rel. 40, Created)
(Rel. 40, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF060565; AAC15232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
                                                                                                                          musculus (Mouse).

Wetazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 28; Conserv
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 34-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1927110;
                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7460;
                                                                                                                                                                                                                                                       INFECTION.
                                                                             16-OCT-2001
                                                                                         16-OCT-2001
16-OCT-2001
                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUGA_APIME
Q08169;
                                                       RW1_MOUSE
070472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                 RESULT 12
                                           RW1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i | | | : :
201 LKAAKRMRPAANWGYYAYPYCYNLTPNQPSAQCEATTWQENDKMSWLFESEDVLLPSVYL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: EXPRESSED IN THE VENOM GLANDS OF WORKER BEES. IT IS ALSO DETECTED IN THE TESTES OF DRONES BUT NOT IN THE QUEEN-BEE VENOM GLANDS OR IN PUPAE.
-!- PTM: TWO DISULFIDE BONDS MAY BE PRESENT.
                                                                                                                                                                                                                            "N-glycan analysis by matrix-assisted laser desorption/ionization mas
spectrometry of electrophoretically separated nonmammalian proteins:
application to peanut allergen Ara h 1 and olive pollen allergen Ole
                                                                                                                                                                                                                                                                                                                                                                                                             ż
                                                                                                                                                                                                                                                                                                                                          Anal. Blochem. 285:64-75(2000).
-!- FUNCTION: MAY PLAY A ROLE IN REPRODUCTION.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-linkages between
                     "The cross-reactivity between bee and vespid hyaluronidases has a structural basis.";
J. Allergy Clin. Immunol. 89:292-292(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Glycosidase; Signal; Glycoprotein; Zymogen; Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0%; Score 75.5; DB 1; Length 382; 21.6%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AWE------GLHENSVRLSRQL---RRILLPL--YEVDDLRD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! SIMILARITY: BELONGS TO FAMILY 56 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl-beta-D-glucosamine and D-glucuronate residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DYFYCWN------TFVENHERT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3E6822E95CA11856 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYALURONOGLUCOSAMINIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D -> S (IN CLONE HYA-2)
N -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WN14_CHICK STANDARD; PRT; 354 AA 042280; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
Jacobson R.S., Hoffman D.R., Kemeny D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                      CARBOHYDRATE-LINKAGE SITE ASN-263.
MEDLINE=20455243; Pubmed=10998264;
Kolarich D., Altmann F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001968; GH 56.
Pfam; PF01630; Glyco_hydro_56; 1.
PRINTS; PR00846; GLHYDRLASE56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44259 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L10710; AAA27730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00846; GLHYDRL.
ProDom; PD003549; GH_56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A47477; A47477.
GlycoSuiteDB; Q08169;
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29
34
115
263
371
37
382 AA;
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Escherichia coll 0157:H7.
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FLRYISDWDLDPGRCYRVT------WFTSWSPCYDCARH----VADFLRGNPNL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 -LTHAMAKACSAGRMERCTCDEAPDLENREAW--QWGGCGDNLKYSNKFVKEFLGRKPNK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDSLLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 SLRIFTARLYFCEDR-----KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galius gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phasianinae;
                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
044BB0539CFD8669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%; Score 75; DB 1; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Indels
     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
WNT-14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF031168; AAC41248.1; -.
InterPro; IPR000970; Wnt_grthfactor.
Pfam; PF00110; Wnt; 1.
SMRT; SM00097; WNTPROTEIN.
PROSITE; PS00246; WNT1; 1.
                                                                                                                    TISSUE=Brain;
MEDLINE=98110581; PubMed=9441749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA; 39813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative
15-JUN-2002 (Rel. 41, Las
WNT-14 protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNR_ECOLI
P37055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Best Local s
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Hnr protein. HNR OR B1235 OR 22011 OR ECS1737. Escherichia coli, and

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                                                                                                                                                                                                                                         Boesl M., Kersten H.; "Organization and functions of genes in the upstream region of tyrr of Escherichia coll: phenotypes of mutants with partial deletion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERZING THE TIME OF STATES AND STATES AND STRAIN-OIST-RIVER TO THE TRAIN-OIST-RIVER THE TRAIN-OIST-RIVER THE TRAIN OIST-RIVER THE TRAIN OIST-RIVER THE STRAIN OF THE STRAIN OF THE STRAIN OF THE STRAIN OF THE STRAIN OIST-RIVER OF THE STRAIN OF THE STRAIN OF THE STRAIN OIST-RIVER OIST-RIVE
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coll K-12."; Science 277:1453-1474(1997).
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MEDLINE-21074935; PubMed-11206551;
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                                                                                         NCBI_TaxID=562, 83334;
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Yano M., Horiuchi T.;
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STRAIN-K12 / MG1655;
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Mau B., Shao Y.;
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DR EWBL, M6603; CA46802.1; DR EWBL, D00708; BAA6103.1; DR EWBL, D007085; BAA6100.1; DR EWBL, AR001781; AA6071. DR EWBL, AR001781; AA6071. DR EWBL, AR001781; AA6071. DR EWBL, PF00707; Response_reg; DR FIR: A36871; A36871. DR FOODM: PD0000039; Response_reg; DR FAMELY SWOODMS RESPONSE_REGULATORY; 1. DR ENCORATE PESONIC ERSPONSE REGULATORY; DR FWOSTIE; PF0001789; RESPONSE REGULATORY; DR FWOSTIE; PF0001789; RESPONSE REGULATORY; DR FWOSTIE; PF000178; DR FWOSTIE; DR FWOSTIE
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MEDLINE=20408890; Pubmed=10950930;
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Homo sapiens (Human).
NCBI_TaxID=9606;
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Q9GZX7
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    protein search, using sw model

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Potal number

Searched:

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Scoring table:

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Muto T., Muramatsu M., Taniwaki M., Kinoshita K., Honjo T.; "Isolation, tissue distribution and chromosomal localization of the human activation-induced cytidine deaminase (hAID) gene."; Genomics 68:85-88(2000). SEQUENCE FROM N.A.

MEDLINE=20460541; PubMed=11007475;
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Catalan N., Forveille M., Dufourcq-Lagelouse R., Gennery A.,
Tezcan I., Ersoy F., Kayserili H., Ugazio A.G., Brousse N.,
Muramatsu M., Notarangelo L.D., Kinoshita K., Honjo T., Fischer A., "Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2)."; Cell 102:565-575(2000). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. TISSUE-B-CELL; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB040431; BAB12721.1; -. EMBL; AB040430; BAB12720.1; -. EMBL; BC006296; AAH06296.1; -. SEQUENCE FROM N.A. Durandy A.;

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_raxID=10090;
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MEDLINE-99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
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EMBL; AF132979; AAD41793.1; -.

MGD; MGI:1342279; Alcda.

InterPro; AR002125; GCMP/Cyt_deam.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN 1.

SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BEB2 CRC64;
InterPro; IPR002125; dcMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 198 AA; 23953 MW; 3C27BB143DB184A9 CRC64;
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ive 0; Mismatches 0;
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                                                                                                      Best_Local Similarity 100.
Matches 198; Conservative
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
88150C2.3 (Putative novel protein similar to APOBECI (Apolipoprotein)
mRNA editing protein) and Phorbolin) (Fragment).
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                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAR45271.1; -.
Interpro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
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InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 384 AA; 46408 MW; 60525DC3B7D903D6 CRC64;
                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) MDS019 (Phorbolin-like protein MDS019).
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                                                    (TrEMBLrel. 16, (TrEMBLrel. 16,
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  PRELIMINARY;
                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 LRAIL 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133
                                                                                                                                          147
                                                                                                                      65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                               11 FLYQFKNVRWAKGRRETYLCYVVK -- RRDSATSFSLDFGYLRN -- -- KNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 FLYQFKNVRWAKGRRETYLCYVVK -- RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                         GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       204;
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                                       Length
                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011739; AAH11739.1; -.
InterPro: IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 190 AA; 22827 MW; DA0584EF75C91CF0 CRC64;
                   79C656F580A40554 CRC64;
                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                       DB 4;
                                      34.0%; Score 369.5; DB 4 44.9%; Pred. No. 1.8e-29; Live 24; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                            33.8%; Score 367.5; DB 4
44.9%; Pred. No. 2.6e-29;
iive 24; Mismatches 64
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                   24285 MW;
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                                                 Local Similarity 44.99
nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 44.9
Matches 79; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phorbolin I protein.
                  204 AA;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Similar to APOBEC
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
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01-MAR-2002
Lipoprotein.
                  SEQUENCE
                                                                                                                                                              125
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                                       Query Match
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                                                           Matches
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Q96F12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ISD---WDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 EPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRILL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                   cells from
SEQUENCE FROM N.A.
Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,
Tu Y., Gu W., Fu G., Huang C.;
"Novel genes expressed in hematopoietic stem/progenitor cells from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQ 175
                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                     Ouery Match 32.6%; Score 354; DB 4; Length 294; Best Local Similarity 43.9%; Pred. No. 9.8e-28; Matches 75; Conservative 26; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003314;
InterPro; IPR002125; dCMP/cyt_deam.
InterPro; IPR002125; dCMP/cyt_deam.
PROSITE; PS00903; cxr_DCMP_DEAMINASES; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 429 AA; 51017 MW; BE44D01380AD7F6E CRC64;
                                                                                                       Myelodysplastic Syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165520; ARF86650.1; -.
InterPro: IPR002125; GMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
SEQUENCE 294 AA; 33363 MW; IB39C7A13D690901 CRC64;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical 51.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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RIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLH 166
                      | :||:|| :: || :|-||||||: :
52 FKFQFRNVEYSSGRNKTFLCYVVEVQSKGGQAQATQGYLEDEHAGAHAEEAFFNTILP-A 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 FDPALKYNVTWYVSSSPCAACADRILKTLSKTKNLRLLILVSRLFMWE----EPEVQAAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 KKLKEAGCKLRIMKPODFEYIWONFVEGEEGESKAFEPWEDIQENFLYYEEKLADIL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99333690; PubMed-10403781;
Liao W., Hong S.H., Chan B.H., Rudolph F.B., Clark S.C., Chan L.;
Liao W., Hong S.H., Chan B.H., Rudolph F.B., Clark S.C., Chan L.;
AROBEC-2, a cardiac- and skeletal muscle-specific member of the
cytidine deaminase supergene family.";
Blochem. Blophys. Res. Commun. 260:398-404(1999).
EMBL; AF161699; AAD45361.1;
MCD; MGI:1343178 APOBEC2.
MCD; MGI:1343178 APOBEC2.
                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.6%; Score 278; DB 11; Length 224; 36.7%; Pred. No. 3.4e-20; Live 26; Mismatches 74; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ34B21.2 (Putative novel protein similar to PART of APOBEC1 (PHORBOLIN 1, apolliopprotein B mRNA editing protein)).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "APOBEC-2, a cardiac and skeletal muscle specific member of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytidine deaminase supergene family.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                         Created)
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                                                                     ENSVRLSRQLRRIL 180
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EHSQDLSGRLRAIL 134
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Matches 65; Conservative
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                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                       APOBEC-2 protein.
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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01-DEC-2001
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   107
                                                                     167
                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                        Q9WV35,
                                                                                                                                                                                                                                                                                            APOBEC2.
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Q9Y235;
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                                                                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 DWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 GYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRN----KNGCHVELLFLRYIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : || : || : || || || || 332 CSLSQEGASVKIMGYKDFVSCWKNFVYSDDEPFKPWKGLQTNFRLLKRRLREIL 385
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
DJ494G10.1 (Novel protein similar to Phorbolin 1 and APOBEC1
(Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1))
                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 315.5; DB 4; Length 48.5%; Pred. No. 3.2e-24; Live 24; Mismatches 40; Indels
                                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017022; AAM17022.1;
InterPro: IPPR002125; dCMP/CYt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 386 AA: 46598 MW; 94C7253BDCC85B22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramsay H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO78641; CA845659.1; -.
InterPro; IPR002125; dCMP/Cyt_deam.
PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16075 MW; C77CB711DDAAA9C0 CRC64;
                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 Score 336.5; DB 4
                                                                                                                                                                                                                                                                                                                                                                          31.0%; Scor.
40.8%; Pred. No. /...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
                                    386 AA
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                    Hypothetical 46.6 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 40.8
Matches 71; Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DJ494G10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                 096AK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09Y4V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
RESULT 8
Q96AK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
09Y4V1
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12;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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Matthews L.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-1999). CAB45276.1; InterPro: IPR002125; dCMP/Cyt_deam. PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN_1.
 mRNA editing protein) and Phorbolin) (Fragment) BK150C2.6.
                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                 SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                     Lipoprotein.
                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UH18
Q9UH18;
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| FKFQFRNVEYSSGRNKTFLCYVVEAQGKGGQVQASRGYLEDEHAAAHAEEAFFNTILP-A 110
                                                                                                                                                                                                                                                                                             70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
                                                                                                                                                                                                                                                                                                                         111 FDPALRYNVTWYVSSSPCAACADRIIKTLSKTKNLRLLILVGRLFMWE----EPEIQAAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : || | | : | : || : || : || || || XQ-EGLCSLSQEGASVKIMGYKDFVSCWKNFVYSDDEPFKFWKGLQTNFRLLKRRLREIL 121
                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BK150C2.6 (Putative novel protein similar to APOBEC1 (Apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                    127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                    11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD
                                                     Liao W., Hong S.-H., Chang B.-J., Rudolph F.B., Clark S.C., Chan L.; "APOBEC-2, a cardiac- and skeletal muscle-specific member of the cytidine deaminase supergene family."; Biochem. Biophys. Res. Commun. 260:398-404(1999).

EMBL, AL011778; CAB4740.1; -.

EMBL, AF161698; AAD45360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              097553;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-BCC-2001 (TrEMBLrel. 19, Last annotation update)
BKL5GC2.10 (Putative novel Phorbolin 1 like protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
                                                                                                                                                                              25.2%; Score 274; DB 4; Length 224; 36.2%; Pred. No. 8.6e-20; Live 25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45273.1; -.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 121
121 AA; 14309 MW; 97FC47DCDD82B247 CRC64;
                                                                                                                                                      224 AA; 25703 MW; CA0905AFAA8C8FA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 270.5; DB 4 45.8%; Pred. No. 9.7e-20; tive 17; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                        MEDLINE-99333690; PubMed-10403781;
                                                                                                                                                                                        Best Local Similaricy
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                         Lipoprotein.
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                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y553
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Q9Y550
ID Q9Y55
AC Q9Y55
DT 01-NO
DT 01-NO
DT 01-MA
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114
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                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YRVIWFISWSPCFSWGCAGEVRAFLQENTHVRLRIFAARIY-----DYDPLYKEALQMLR
                                                                                                                                                                                 55 CHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLY
                                                                                                                                                                                                         10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09Y554;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BK150C2.9 (Putative novel Phorbolin 1 like protein) (Fragment).
                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BK15002.1 (Putative novel Phorbolin 1 like protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || |::|||::||| DAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQALSGRLRAIL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                         Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matthews L.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022318; CAB45269.1; -.
                                          5DC969AE3ED348D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 111 AA; 13006 MW; EF8922AEBFFA7028 CRC64;
                                                                                                                                                                                                                                                                           115 FCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFV 152
                                                                                                                                                                                                                                                                                                     67 YFWDTDYQ-EGLRSLSQEGASVEIMGYKDFKYCWENFV 103
                                                                                  23.7%; Score 257.5; DB 4; 50.0%; Pred. No. 1.7e-18; tive 13; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 251; DB 4;
46.4%; Pred. No. 8.2e-18;
tive 20; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                103 103
103 AA; 12146 MW;
                                                                                                            Best_Local Similarity 50.0%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.4%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
\frac{1}{103}
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Q9Y554
ID Q9Y55
AC Q9Y55
DT 01-NO
DT 01-NO
DT 01-DE
DE BK150
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3

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GN BK150C2.9.

S Homo sapiens (Human).

CC Manmalia: Butheria; Drimates; Catarrhini; Hominidae; Homo.

CM Annmalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

CM Annmalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

RN CELTAXID—9606;

RN (131 TaxID—9606;

RN (131 TaxID—9606;

RN Anthews L.;

RN SEQUENCE FROM N.A.

RA MATCHEWS L.;

RN SUDMITTER 121 121 121

BN SEQUENCE 121 AA; 14714 MW; BBFE133AACBE6D59 CRC64;

NON_TER 121 121 121

SO SEQUENCE 121 AA; 14714 MW; BBFE133AACBE6D59 CRC64;

OUMERY MATCH

BOST LOCAL SIMILARIY 39.3%; Pred. NO. 1e-16;

MATCHES A8; CONSERVATIVE 19; Mismatches 54; Indels 1; Gaps 1;

OUS SEQUENCE 121 AA; 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
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Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 2, Appli

US-08-680-326-40
US-08-080-255-7
US-08-08-05-7
US-08-061-376-5
US-08-061-376-5
US-09-085-259-2
US-09-092-315-2
US-09-092-315-6
US-09-092-315-6
US-09-092-315-6
US-08-356-034-2
US-08-933-891-2

Run on:

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366
110994
14000
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13969
5333
1727
1127
11176
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11176
11176
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TOPOLOGY: linear
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LIBRARY: PROSTUT09
      Sequence 1, Appli
Sequence 3, Appli
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Sequence 5, Appli
                                                                                                                                                              (without alignments) 224.067 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
Sequence 1,
Sequence 1,
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                                                                                                                                                                                                                   US-09-966-880A-8
1086
1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL
                                                                                                                                       June 14, 2003, 18:08:03; Search time 26 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-395-3
US-08-687-895-4
US-08-816-214-4
US-09-040-482-4
US-09-158-395-4
US-08-158-682A-4
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-015-203-2
US-08-687-895-5
US-08-816-241-5
US-09-040-482-5
US-09-128-395-5
US-09-092-315-3
                                                                                                                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
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Maximum DB seq length: 200000000
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Sequence:
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Result Š

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ALIGNMENTS

KESULT 1
US-08-816-241-1
Sequence 1, Application US/08816241
Sequence 1, Application US/08816241
Setent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TILLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.0%; Score 369.5; DB 1;
44.9%; Pred. No. 1.2e-35;
tive 24; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICALLO.

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 9F-0239 US
TELECOMMUNICATION INFORMATION:
TELEFAN. 415-855-055
TELEFAN. 415-854-4166
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.9
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LIBRARY: PROSTI
; CLONE: 1646823
US-08-816-241-1
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Sequence 56, Sequence 56, Sequence 56, Sequence 56, Sequence 56, Sequence 56, Sequence 6, P

US-08-474-853-56 US-09-166-205B-56 PCT-US94-02629-56 US-08-488-305A-6

US-08-180-209B-56

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70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 FDPALRYNVTWYVSSSPCAACADRIXKTLSKTKNLRLLILVGRLFMWE----EPEIQAAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD 69
                134 GLRSLSQEGVAVEIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 12;
                                                                                                       Sequence 1, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
25.0%; Score 271; DB 1; L.
Best Local Similarity 35.8%; Pred. No. 6e-24;
Matches 63; Conservative 25; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASKSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
NUMBERY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09040482
Patent No. 5916556
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 222 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide IMMEDIATE SOURCE:
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LIBRARY: MUSC...
57953
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TOPOLOGY: lin
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                                                                   65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                          FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                               11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.0%; Score 369.5; DB 3;
44.9%; Pred. No. 1.2e-35;
tive 24; Mismatches 64;
                                                                                                                                                                                                                                                             Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: GOli, Surya K.
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0239 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFLIANT DATE:
FILING DATE:
ATTORNATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 44.99
Matches 79; Conservative
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MEDIUM TYPE: Diskett
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LIBRARY: PROST
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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
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46.4%; Pred. No. 2.8e-21;
Live 17; Mismatches 32; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 DAGAQVSIMTYDEFEYCWDTFVXRQCCPFQPWDGLEEHSQALSGRLRAIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08816241

Patent No. 5804185

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSLSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
                                                                                                                                                                                                    PF-0109 US
                                                                                                 APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Filed Herewith
                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                          116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.49
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank
                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIALL
LIBRARY: Genberr
Train 436941
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-816-241-3
                                                                                                                                                                                                                                                                                                                            LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 LDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPE---GL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKN-GCHVELLFLRYISDWD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 RRLHRAGVQIAIMTFKDYFYCWNTFVENHE---RTFKAWEGLHENSVRLSRQLRRI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 271; DB 2; Length 222;
; Pred. No. 6e-24;
25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hankins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0109 US
                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASLEDQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT.

NAME: B1111ngs, Lucy J.

REGISTRATION NUMBER: 36,749

REFRENCE/DOCKET NUMBER: PF-O

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.0%;
Best Local Similarity 35.8%;
Matches 63; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COMPUTER READABLE FORM:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: MUSCNOT1
CLONE: 57953
                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Por
CITY: Palo Alto
                                                                                                                   U.S.
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                                                                                                                 COUNTRY: U
ZIP: 94304
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10; Gaps

Indels

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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
                                                                                         131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                               62 DAGAQVSIMIYDEFEYCWDIFVYRQCCPFQPWDGLEEHSQALSGRLRAIL 111
                     Pred. No. 2.8e-21;
7; Mismatches 32;
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARR: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
                                                                                                                                                                                                                                              US-09-128-395-3
; Sequence 3, Application US/09128395
; Patent No. 6087108
                     Best Local Similarity 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                   51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: General Library 436941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-687-895-4
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                                       Matches
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                                                                                                                                                                                                                                                                                                                   32; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                   22.6%; Score 245; DB 1; Length 116; 46.4%; Pred. No. 2.8e-21; tive 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09040482
Patent No. 5916556
GENERAL INFORMATION
APPLICANT: An-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
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SOFTWARE: FASTED VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
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APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                    : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 amino acids
                                                                                                                                                                                                                                                           51; Conservative
                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                      LIBRARY: GenBank
CLONE: 436941
                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
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                                                                                                                                                                                         US-08-816-241-3
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                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 51
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                                                                                                                                                                        CLONE:
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76 YRVTWFTSWSPCYD--CARHVADFLRGNPNLSLRIFTARLYFCEDRKAEP---EGLRRLH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DAGAQVSIMTYDEFEYCWDTFVYRQGCPFQPWDGLEBHSQALSGRLRAIL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 RAGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.6%; Score 245; DB 3;
46.4%; Pred. No. 2.8e-21;
tive 17; Mismatches 32,
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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DB 2; Length 116;

22.6%; Score 245;

Query Match

us-09-966-880a-8.rai

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PF-0239 US
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                      236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 19.99
Best Local Similarity 34.99
Matches 44; Conservative
                                                                                                                                                                  FILING DATE: Filed Her
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: GenBank
CLONE: 11777906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 CWRNFV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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APPLICANT: Gol1, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/687,895
FILING DATE: Filed Herewith
ATTONNEY,AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0109 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
Sequence 4, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 amino acids
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Best Local Similarity 34.9%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: pepi
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ZIP: 94304
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87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
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Patent No. 5916556
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19:9%; Score 216.5; DB 1; 34.9%; Pred. No. 1.7e-17;
OPERATING SYSTEM: DOS
SOFWARE: FSSLESO, for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
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Gaps

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87 CYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFY 146
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م
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Davidson, Nicholas O. TITLE OF INVENTION: Apollpoprotein B RNA Editing Protein: TITLE OF INVENTION: Composition and Method NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.3%; Score 210; DB 1; Length 236; 35.6%; Pred. No. 9.7e-17; tive 28; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: ARNOLD WHITE & DURKEE STREET: 321 No. 5434058th Clark Street, Suite 800 STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08158682A
Patent No. 5434058
GENERAL INFORMATION:
                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COOLIEY, ROHAID B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 4:
                                                                                                LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 35.66
Matches 48; Conservative
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                                                                                                                                                     TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                       LIBRARY: GenBank
CLONE: 11777906
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Best Local Similarity
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: USA
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CLASSIFICATION:
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US-08-158-682A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 RRDSATSFSLDFGYLR----NKNGC-HVELLFL-RYISDWDLDPGRCYRVTWFTSWSP
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
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Best Local Similarity 34.9%; Pred. No. 1.7e-17;
Matches 44; Conservative 31; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: GOLI, SULYA K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Blllings, Lucy J.

RECISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: 9F-0109 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-85-055

INFORMATION FOR SEQ ID NO: 4:

SEGUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TYPE: amino acid

STRANDEDESS: single
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/687,895
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Patent No. 6087108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            NOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                  GenBank
                                                                                                                                                                                                                                                                                                                         AMEDIAL
LIBRARY: General
AME: 1177798
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                                                                                                                                                                                                                                                                                         TOPOLOGY: II
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STATE:
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                                    RRETYLCYVVK----RRDSATSFSLDFGYLRNKNGC-HVELLFL-RYISDWDLDPGRCYR 77
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                                                                                                78 VTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRKAEPEGLRRLHRAGVQIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davidson, Nicholas O.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: ARNOLD, WHITE & DURKEE
321 No. 5434058th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 198; DB 1; L 32.9%; Pred. No. 2.4e-15; Live 24; Mismatches 62;
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NAME: COOLLEY, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,682A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08158682A Patent No. 5434058
                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 IMTFKDYFYCWNTFV 152
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 32.9
Matches 56; Conservative
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MOLECULE TYPE: peptide
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Sequence 2, Application US/08015203
Patent No. 5550034
GENERAL INFORMATION:
APPLICANT: Teng, Babie
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ARDDRESSEB: ARROLD, WHITE & DURKEE
STREET: 321 No. 5550034th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.2%; Score 198; DB 1; Length 229; 32.9%; Pred. No. 2.4e-15; Live 24; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:069
TELECOMMUNICATION INFORMATION:
TELEPHONE /2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/015,203
FILING DATE: 19930209
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coolley, Ronald B REGISTRATION NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 229 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1993020
CLASSIFICATION: 435
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Best Local Similarity
Matches 56; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Search completed: June 14, 2003, 18:12:28 Job time: 27 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 14, 2003, 18:09:18; Search time 21 Seconds

(without alignments)
1008.062 Million cell updates/sec

Title: US-09-966-880A-8
Perfect score: 1086
Sequence: 1 MDSLLMNRRKFLYQFKNVRW......ILLPLYEVDDLRDAFRTLGL 198
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643
Minimum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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7: Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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9: Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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13: Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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14: Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

Published_Applications_AA:*

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 174, Appl Sequence 136, Appl Sequence 36, Appli Sequence 3, Appli Sequence 5, Appli Sequence 14, Appli Sequence 14, Appli Sequence 16, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli
SUMMARIES	US-09-966-880A-8 US-09-966-880A-2 US-09-729-74-174 US-09-925-300-1639 US-09-966-880A-36 US-09-864-761-38853 US-10-120-319-3 US-10-120-319-3 US-10-120-319-5 US-10-153-668-164 US-10-153-668-164 US-10-153-668-164 US-09-847-208-25 US-09-910-186A-8 US-09-910-186A-8 US-09-910-186A-8 US-09-913-52-5 US-10-120-319-2 US-10-120-319-2
DB	
% Query Match Length DB	1198 1198 1198 1222 1224 1224 1236 1338 1382 1382 1382 1382 1382 1382 1382
% Query Match	000 000 000 000 000 000 000 000 000 00
Score	1088 369.5 211 844 810 80 77.5 77.5 77.5 77.5 71.5 69 69 69
Result No.	100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Sequence 1041, Ap Sequence 762, App Sequence 6, Appl1 Sequence 6, Appl1 Sequence 18, Appl1 Sequence 17, Appl Sequence 17, Appl Sequence 5, Appl1 Sequence 3, Appl1 Sequence 31, Appl Sequence 287, Appl Sequence 27, Appl1 Sequence 27, Appl1 Sequence 26, Appl1 Sequence 28, Appl1 Sequence 58, Appl Sequence 127, Appl Sequence 180, Appl Sequence 58, Appl Sequence 180, Appl			Length 198; Indels 0; Gaps 0;	SFSLDFGYLRNKNGCHVELL 60	NPNLSERIFTARLYECEDRK 120 	AWEGLHENSVRLSROLRRIL 180
US-09-764-868-1041 US-09-925-302-762 US-10-120-319-6 US-10-120-319-6 US-10-120-319-6 US-09-733-524-18 US-09-733-524-18 US-09-733-524-18 US-09-864-761-42836 US-09-864-761-42836 US-09-864-761-42836 US-09-864-761-42836 US-09-981-220-287 US-09-981-220-287 US-09-981-220-287 US-09-815-996A-33 US-09-815-996A-3 US-09-811-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-132-565 US-09-981-137-5 US-10-114-893-127 US-09-880-748-1480 US-10-125-540-353 US-10-113-313-437	ALIGNMENTS	ESSULT 1 Sequence 8, Application US/09966880A Patent No. US20020164743A1 GENERAL INFORMATION: APPLICANT: HONJO, Tasuku APPLICANT: Muramatsu, Masamichi TTILE OF INVENTION: NOVEL CYTIDINE DEAMINASE FILE REFERENCE: 06501-088001 CURRENT APLICATION NUMBER: US/09/966,880A CURRENT PILING DATE: 2000-03-28 PRIOR APPLICATION NUMBER: PT/JF00/01918 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR FILING DATE: 1999-12-27 PRIOR APPLICATION NUMBER: JP 11-371382 PRIOR FILING DATE: 1999-06-24 PRIOR FILING DATE: 1999-06-24 PRIOR FILING DATE: 1999-03-29 NUMBER OF SEQ ID NOS: 36 SEQ ID NO 8 LENGTH: 198 TYPE: PRT	; Score 1086; DB 9; ; Pred. No. 3e-108; 0; Mismatches 0;	MDSLLMNRRRFLYQFRNVRMAKGRRETYLCYVVRRDSATSFSLDFGYLRNKNGCHVELL 	FLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYFCEDRK 	AEPEGLRRLHRAGVQIAIMTEKDYFYCWNTFVENHERTFKAWEGLHENSVRLSRQLRRIL
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		tion US/099 64743A1 1 asuku tsu, Masami, tsu, Masami, 501-088001 N NUMBER: Up 2000-03-28 2000-03-28 1099-06-24 1099-06-24 1099-06-24 1099-06-24 1099-06-24 1099-06-24 1099-06-24 1099-06-24	100.0% 100.0% ative	RRKFLYQFKNV] RRKFLYQFKNV]	WDLDPGRCYRV 	RLHRAGVQIAII RLHRAGVQIAII
688 688 688 688 688 688 688 688		18-SULT 1 18-O-966-880A-8 18-O-966-880A-8 18-O-966-880A-8 18-O-966-880A-8 18-O-966-880A-8 18-O-966-880A-8 18-O-96-880A-8 18-O-996-880A-8 18-O-99-96-880A-8 18-O-99-96-880A-8 18-O-99-96-880A-8	atch sal Similarity 198; Conserv	1 MDSLLMN MDSLLMN	61 FLRYISD 61 FLRYISD	121 AEPEGLR 121 AEPEGLR
0 1 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2		RESULT 1 US-09-966-880A-8 Sequence 8, App Sequence 8, App GENERAL INPORM APPLICANT: M APPLICANT: M TITLE OF INVE FILE REFERENC CURRENT APPLICANT CURRENT APPLICANT PRIOR PILING PRIOR PILING PRIOR PILING PRIOR PILING PRIOR FILING PRIOR PRIOR FILING	Query Match Best Local S Matches 198	QY Db	QY Db	Qy Db
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HVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSLRIFTARLYF 115
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                                                                                                                                                                                                                                                                                                                                                6 MNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLD--FGYLRNK-----NGC 55
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM PETER REPERENCE: 6055-64X
CURRENT APPLICATION NUMBER: 02/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               11 FLYQFKNVRWAKGRRETYLCYVVK--RRDSATSFSLDFGYLRN----KNGCHVELLFLRY
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                                                                                                                                                                                                                                                                       Length 384;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE FINATION: Nucleic Acids, Proteins and Antibodies
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                       35.9%; Score 390; DB 10; 44.9%; Pred. No. 1.6e-33;
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                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1639, Application US/09925300 Patent No. US20020151681A1
                                                                                                                                                                                                                                                                                                           31;
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44.9%;
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SOFTWARE: PatentIn Ver. 2.(
                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-925-300-1639
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Matches 83; Conserv
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Best Local Similarity
Matches 79; Conserv
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                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PTI/180399
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR FILING DATE: 1999-12-27
PRIOR PILING DATE: 1999-16-27
PRIOR FILING DATE: 1999-06-37
PRIOR FILING DATE: 1999-06-37
PRIOR FILING DATE: 1999-06-37
PRIOR FILING DATE: 1999-06-37
PRIOR FILING DATE: 1999-06-329
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASLED for Windows Version 4.0
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Steininger II, Robert J.
Spaulding, Vikki
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Clark, Hilary
Fechtel, Kim
Genetics Institute, Inc.
                                                                                                                                                 Sequence 2, Application US/09966880A
Patent No. US20020164743A1
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LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
                 181 LPLYEVDDLRDAFRTLGL 198
                                     LPLYEVDDLRDAFRMLG 197
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APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward
APPLICANT: Collins-Racie, Li
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Merberg, David
APPLICANT: APPLICANT: Jeacy, Mauricel
APPLICANT: Steininger II, Ro
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Treacy, Maurice
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Matches 183; Conservative
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ORGANISM: Mus musculus
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                                                                                                          RESULT 2
US-09-966-880A-2
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN MAGNE ASIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN FERTL LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 4.1
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/704,203
PRIOR APPLICATION NUMBER: US 09/704,203
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 38853
LENGTH: 51
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Patent No. US20020164749A1
GENERAL INFORMATION:
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ORGANISM: Helicobacter pylori
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 20; Conserva
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US-09-864-761-38853
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LENGTH: 440
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| Patent No. US20020048763a1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G.
| APPLICANT: Hanzel, David R.
| APPLICANT: Chen, Wensheng
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
| FILE REFERENCE: Aeonica.x-1
| CURRENT FILING DATE: 2001-05-23
| PRIOR APPLICATION NUMBER: US 60/207,456
| PRIOR PILING DATE: 2000-02-04
| PRIOR PILING DATE: 2000-08-03
| PRIOR FILING DATE: 2000-09-27
| PRIOR FILING DATE: 2000-10-04
| PRIOR FILING DATE: 2000-10-04
| PRIOR FILING DATE: 2000-10-04
| PRIOR FILING DATE: 2001-03-27
| PRIOR FILING DATE: 2001-03-27
| PRIOR FILING DATE: 2001-03-37
| PRIOR FILING DATE: 2001-03-37
| PRIOR FILING DATE: 2001-03-30
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APPLICANT: HONJO, TASUKU
APPLICANT: HONJO, TASUKU
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28
PRIOR PELICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PT 11-371382
PRIOR FILING DATE: 1999-12-7
PRIOR FILING DATE: 1999-12-7
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 229
                                                                                                                                                                                     Sequence 36, Application US/09966880A
Patent No. US20020164743A1
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Matches 49; Conservative
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146 EQEYCYCWRNFV 157
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US-09-966-880A-36
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                                                                                                                    US-09-966-880A-36
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221 NKNEFLSQYK------FNLCF------ENSQGYGYVTEK-----IIDAYFS 254
                                                                                                                                                          67 D-----ADFLRGNPNLSLR 107
                                                                                                                                                                                            255 HIIPIYWGSPSVAKDFNPKSFVNVHDFKNFDEAIDYVRYLHTHPNAYLDMLYENP---LN 311
                                                                                                                                                                                                                                 108 IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVEN----HERTFKAWE 163
                                                                                                                                                                                                                                                                 312 TLDGKAYFYQD-------LSFKKILDFFKTILENDTIYHNNFVFYR 351
                                                                               7 NRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-----W-----DLDPGRCYRVTWFTSWSPCYDCARHV-----ADFLRGNPNLSLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVEN----HERTFKAWE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09733524
Patent No. US20020068347A1
GENERAL INFORMATION
APPLICANT: The Governers of the University of Alberta, a Canada Corporation
APPLICANT: Taylor, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INPORMATION: USLOCATION 494911

APPLICANT: Taylor, Diane E.
APPLICANT: Taylor, Diane E.
TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLITRANFERASE
FILE REFERENCE: 07254/049001
FILE REFERENCE: 07254/049001
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: USLOCATION NUMBER: 09/092,315
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0

LENGTH. 476
                                                     Gaps
             DB 9; Length 440;
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                                                 Indels
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                                                 61;
7.5%; Score ...,
20.7%; Pred. No. 2;
**ive 22; Mismatches (
                                                                                                                                                                                                                                                                                                           164 GLHENSVRLSRQLRRILLPLYEVDDLRDAFRTL 196
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----PLVSIDDLRADYNNL 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLHE-----PLISIDDLR 368
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10120319
Patent No. US20020164749A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Helicobacter pylori
US-10-120-319-5
 Query Match 7.5
Best Local Similarity 20.7
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 20.89
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                                                                                                                                                                                                                                                                                                                                                  352 DLNE----
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US-09-733-524-15
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Sequence 14, Application US/10080960
| Sequence 14, Application US/20020197695A1
| CENERAL INFORMATION:
| APPLICANT: Milennium Pharmaceuticals, Inc.
| APPLICANT: Mayers, Rachel
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
| TITLE OF INVENTION: MUMBER: US/10/080,960
| CURRENT FILING DATE: 2001-10-19
| PRIOR PILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING AND TITLE OF INVENTION: EXPRESSION THEM
FILE REFERENCE: 07254/049002
CURRENT APPLICATION NUMBER: US/09/733,524
CURRENT APPLICATION NUMBER: 09/092,315
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE FEASES for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 NKSEFLSQYK------FNLCF------ENSOGYGYVTEK-----ILDAYFS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 D-----W------DLDPGRCYRVTWFTSWSPCYDCARHV-----ADFLRGNPNLSLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 HTIPIYWGSPSVAKDFNPKSFVNVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENP---LN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 IFTARLYFCEDRKAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVEN----HERTFKAWE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 NRRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Helicobacter pylori fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
7.4%; Score 80; DB 10;
Best Local Similarity 20.8%; Pred. No. 2.8;
Matches 43; Conservative 21; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 GLHENSVRLSRQLRRILLPLYEVDDLR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 DLHE------368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (0)...(0)
; OTHER INFORMATION: Strain 26695A
US-09-733-524-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 15
LENGTH: 476
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                                                                                                                                                                                                         249 EKIQKSKGDDATLPSFRLPKDKTGTTRIGDLAPQDMKKVCHLALIELTALYDVLGIELKQ 308
                                                                                                                                                                                                                                                                                                   GRCYRVTWFTSWSPCYDCARHVADFLRGNPNLSL-RIFTARLYFCEDRKAEPEGLRRLHR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AGVQIAIMTFKDYFYCWNTFVENHERTFKAWEGL--HENSVRLSRQLRRILLPLYEVDDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638 OSEVLFLLONLTLOEITFSFCRLFEKRPAOFLPEMVAAMKGNSTLKGLRLPGNRLGNAGL 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EPEGL----RRLHRAGVQIAIMTFKDYFYCWNTFV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----WGRGA 741
                                                                                                                                               16 KNVRWAKGRRETYLCYVVKRRDSATSFSLDFGYLRNKNGCHVELLFLRYISD---WDLDP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCYVVKRRDSATSFSL....-DFGY...-LRNKNGCHVELLFLRYISDWDLDPGRC 75
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Gaps
                                                                                 15;
       DB 9; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 LALADVFSEDSSSSLCQLDISSNCIKPDGLLEFAKRLER----
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                                                                             94;
7.1%; Score 77.5; DE 22.5%; Pred. No. 7.8; ative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 11; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: MURAMATSU, Shuji
APPLICANT: MURAMATSU, Shuji
APPLICANT: MURAMATSU, Shuji
APPLICANT: SHIZAMA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/218,403
PRIOR APPLICATION NUMBER: US 60/318,403
PRIOR APPLICATION NUMBER: US 60/318,738
PRIOR APPLICATION NUMBER: US 2001-157043
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-00-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 164, Application US/10153668 Publication No. US20030092616A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
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                                                                         Conservative
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US-10-153-668-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | : :
K-AFOAV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDAFRTL 196
                                  Local Similarity
tes 42; Conserv
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SEQ ID NO 164
LENGTH: 790
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Best Local S
Matches 51
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   Query Match
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APPLICANT: LADUNGA, Steven et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: SOLATED HUMAN SECRETED PROTEINS,
TITLE DE INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00818CON
CURRENT APPLICATION NUMBER: US/10/265,593
CURRENT PILING DATE: 2002-10-08
PRIOR FILING DATE: 2000-09-11
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                Sequence 25, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shang, Ke
APPLICANT: Zhang, Ke
TILLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TILLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT FILIAG DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
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                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Apis mellifera (Honeybee)
US-09-847-208-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/10265593; Publication No. US20030049789A1; GENERAL INFORMATION:
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Matches 42; Conserve
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Matches 36; Conserv
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US-10-265-593-4
US-09-847-208-25
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Search completed: June 14, 2003, 18:12:57 Job time: 23 secs
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APPLICANT: BACHMANN, Heinrich
APPLICANT: BRUGGER, Roland
APPLICANT: BRUGGER, Roland
APPLICANT: BRUGGER, Roland
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WIRTZ, Gabriele M
APPLICANT: WYSS, Marian
APPLICANT: WYSS, Marian
APPLICANT: WYSS, Marian
APPLICANT: WYSS, Markus
ITILE OF INVENTION: BETA, BETA, CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID
ITILE OF INVENTION: SEQUENCES CODING THEREFOR AND THEIR USE
CURRENT APPLICATION NUMBER: US/10/053,192
CURRENT APPLICATION NUMBER: 103182.0
FRIOR APPLICANTON NUMBER: 103382.0
FRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
57 VELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCAR-----HVADFLRGNPNLSLRI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 VKINLFKFLSSWSL------WGANYMDCFESFTNETMGVWLHIADKKR------ 287
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                                                                105 SLRIFTARLYFCEDR-----KAEPEGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHE 156
                                                                                                 51;
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Fublication No. US20030009025A1

GENERAL INFORMATION:

APPLICANT: U.S. Army Medical Research & Material Command

TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM

TITLE OF INVENTION: NEUROTOXIN

FILE REFERENCE: A33626-A 057525.0107

CURRENT APPLICATION NUMBER: US/09/910,186A

CURRENT FILING DATE: 2001-07-20

PRIOR PILING DATE: 2000-05-12

PRIOR PLICATION NUMBER: 09/611,419

PRIOR FILING DATE: 2000-07-106

PRIOR FILING DATE: 1999-05-12

PRIOR APPLICATION NUMBER: 60/133,865

PRIOR FILING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12

PRIOR PLING DATE: 1999-05-12
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Best Local Similarity 20.8%; Pred. No. 26;
Matches 31; Conservative 25; Mismatches
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                                                                                                                                                                                                                           Sequence 5, Application US/10053192
Publication No. US20030087336A1
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; ORGANISM: BOVINE
US-10-053-192-5
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                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Synthetic construct based on Clostridium botulinum corner INFORMATION: sequence US-09-910-186A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 440;
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PRIOR APPLICATION NUMBER: 60/133,868
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1993-09-11
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
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AF529833 Mus muscu
AF529833 Mus muscu
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AF529831 Homo sapi
AF529825 Homo sapi
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AF529837 Homo sapi
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AF52984 Homo sapi
AF52984 Cricetulu
AF52984 Homo sapi
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AB040431 Homo sapi
AF529815 Homo sapi
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AF529812
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                                          em_htg_inv:*
em_htg_other:*
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em_htgo_hum:*
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                      em_htg_hum: *
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                                                                                     em_htg_mus:*
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Match Length DB
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-Q-/Cgn2_1/USPTO_spool/US09966880/runat_14062003_175645_16271/app_query.fasta_1.391
-Q-/Cgn2_1/USPTO_spool/US09966880/runat_14062003_175645_16271/app_query.fasta_1.391
-DB-GenEmbl. QFRWT=fastap -SUFFIX=Plo.rge -MINMATCH=0.1 -LOOPCIx=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=blts -START=1 -END=-1 -MATRIX=00 -THR_MIN=0 -MAXLEN=200000000
-USER-USO9966880_eCGN_1_1_2496_erunat_14062003_175645_16271 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WANN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2318.855 Million cell updates/sec
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                                                                                                                                             June 19, 2003, 11:55:51; Search time 2485 Seconds
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                       nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext
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AF529826 596 bp mRNA linear PRI 19-AUG-2002
Homo sapiens clone Ramos 12 AID (AID) mRNA, partial cds.
AF529826
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NWSCHLENSVRLSRQLRRILLFLYEVDDLRDAFRTLGL"
155 9 151 151
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/gene="AID"
/note="integrated into Burkitt's lymphoma cell line Ramos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Unpublished
Unpublished
Unpublished
Wartin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
Location/Qualifiers
I. 596
/Organism="Homo Sapiens"
/db_xref="tamos 12"
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                               non-B
     301 AACCCCAACCTCAGTCTGAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG
                                                                                          141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
                                                                                                         1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
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Catarrhini; Hominidae; Homo.
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Somatic hypermutation of the AID transgene in B cells
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Eukaryota; Metazoa; Chordata;
Mammalia: Butheria; Primates;
1 (bases 1 to 596)
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/gene="AID"
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NLSLRIFTARLFYCEDRKAEPEGLERRHARGYQIAIMTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFFLGL"
163 c 155 g 150 t
                   linear PRI 19-AUG-2002 partial cds.
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Catarrhini; Hominidae; Homo.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                          1 (bases 1 to 596)
Martin,A. and Scharff,M.D.
Somatic hypermutation of the AID transgene in B cells and non-B
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1. .>596
/gene="AID"
/note="AID"
/codon_start=1
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                 (AID) mRNA
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Mismatches:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 9"
1. >>596
                596 bp
9 AID (
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Mammalla; Eutheria; Primates;
                         Homo sapiens clone Ramos
AF529823
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                                                        AF529823.1 GI:22297233
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Best Local Similarity:
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Homo sapiens, activation-induced cytidine deaminase, clone MGC:12911 IMAGE:4054915, mRNA, complete cds.
BC006296
BC006296.1 GI:13623400
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1837)
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Matches:
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/product="AID"
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Sciurognathi; Muridae; Murinae; Mus
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USA
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Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
Location/Qualifiers
                                                                                                                                                                                                                                                                                              596 bp mRNA linear SYN 19-Au clone 10 transgenic Homo sapiens AID (AID) mRNA,
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/db_xref="taxon:10090"
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/db_xref="taxon:9606"
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Martin, A. and Scharff, M.D Somatic hypermutation of Unpublished
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/codon_start=1
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Mammalla; Eutheria;
1 (bases 1 to 596)
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Location/Qualifiers
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Muto,T., Levy,Y., Geissmann,F., Plebani,A., Sanal,O.,
Catalan,N., Forveille,M., Dufourcq-Lagelouse,R., Gennery,A.,
Tezcan,I., Ersoy,F., Kayserili,H., Ugazio,A.G., Brousse,N.,
Muramatsu,M., Notarangelo,L.D., Kinoshita,K., Honjo,T., Fischer,A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      PheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrp
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Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Direct Submission
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens cDNA to mRNA.
Homo sapiens
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AB040431.1 GI:9988409
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77. .673
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DEGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDGRHYADFLRGNP
NLSLRIFTARLYFCEDRKAEPBGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
NWEGLHENGVRLSFOLDLRDLRDLRDAFRTLGL"
387 c 421 g 499 t
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    http://www.nisc.nih.gov/
Contact:
    nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjanih,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Gunn,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 17 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9988409. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60
                                 Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rbian Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:

http://www.nisc.nih.gov/
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/clone="MGC:12911 INAGE:4054915"
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2 (bases 1 to 596)
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, T
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Ci
1 (bases 1 to 596)
Martin, A. and Scharff, M.D.
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Homo sapiens clone Ramos
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596 bp mRNA linear SYN 19-AUG-2002
Mus musculus clone 8 transgenic Homo sapiens AID (AID) mRNA,
AF529835
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DEGYLRNKNCCHVELLFLRYISDWDLDPGRCYRVTWRTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPBGLRRLHRAGVQIAIMTFKDYFYCWNTFVENHERTFK
WARGCHBRNSVRLSCHRILLDLYFVDDLRDAFRTLGL"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:9606"
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/db_xref="GI:22297258"
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Martin, A. and Scharff, M.
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/product="AlD."
/protein_id="AaM95420.1"
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DFGYLRNKGCHPELLELRYISDWDLDPGRCYRYTWFTSWSPCYDCARHYADFLAGNP
NLSLRIFTARLYFCEDRKAEPEGLRRHRAGVOIAINTFKDYFYCWNTFVENHERTFK
AWEGLHENSVRLSRQLRRILLPLYEVDDLRDAFRFLGL"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA
cells
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                                     1 (bases I to 596)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B and non-B
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/transgenic
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/db_xref="taxon:9606"
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/clone="6"
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FEATURES Location/Qualifiers 1596 /organism="Mus musculus" /db_xref="taxon:10090" /cell_type="hybridoma Pl-5" /transgenic 1596 /organism="Homo sapiens" /db_xref="taxon:9606" 1>596 1>596	/gene="AID" 1. >>56 /gene="AID" /codon_start=1 /product="AID" /protein_id="AAM95417.1" /db_xref="GI:22297248" /translation="MDSILMNRRKFLYOFKNVRWAKGRRETYLCYVVKRRDSATSFSL	DFGYLRNKNGCHVELLFLRYISDWDLDFGRCYRVT NLSLRIFTARLYFCEDRKAEPEGLRRLHRAGYOIA AWEGLHENSVRLSRQLRRILPLYEVDDLRDAFRT COUNT 126 a 164 c 155 g 151 t LN INMENT SCOTES: 1.04e-108 Length: 59 . No.:	1 t Similarity: 1 ocal Similarity: 9 Watch: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 MetaspSerLeuLeuMetasnargargLysPheLeuTyrGlnPheLysasnValargTrp 20	41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60		AlaGluproGluGlyLeubrgArgLeuHisArgAlaGlyValClnIlealaileMetThr
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Mus musculus clone 11 transgenic Homo sapiens AID (AID) mRNA, complete cds.
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Sciurognathi; Muridae; Musimae; Mus
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Martin, A. and Scharff, M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA Location/Qualifiers
                                                                                                                                                                                              AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
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Somatin, Angermutation of the AID transgene in B and non-B (Unpublished
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Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, USA 1. 596
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                  2 (bases I to 596)
Martin,A. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, I300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U.
Location/Qualifiers
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                                                                                                          Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (2008) 1 (2008)
Martin, A. and Scharff, M.D.
Somatic hypermutation of the AID transgene in B cells and
                                                                                                                                                                          AF529825 596 bp mRNA linear
Homo sapiens clone Ramos 11 AID (AID) mRNA, partial
AF529825
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/db_xref="taxon:9606"
/clone="Ramos 11"
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DFGYLRNKNGCHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRGNP
NLSLRIFTARLYFCEDRKAEPBGLRRLHRAGVQIAINTFKDYFYCWNTFVENHERTFK
WMEGJHENSVRLLSDLRILLDLYEVDDLRDAFRTLGL"
165 c 155 9 150 t
                                                                                                                                                                                                                                                                /gene="AID"
/note="integrated into Burkitt's lymphoma cell line Ramos"
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USA
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2 (bases 1 to 596)
Martin, a. and Scharff,M.D.
Direct Submission
Submitted (17-JUL-2002) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave. Chanin 404, Bronx, NY 10461, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr
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                                                                  Martin,A. and Scharff,M.D. Somatic hypermutation of the AID transgene in B cells and
                                     Craniata; Vertebrata; E
Catarrhini; Hominidae;
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/protein_id="AAM95409.1"
/db_xref="GI:22297232"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ramos 8"
                                  Chordata; (Primates; (
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/gene="AID"
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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41 SerPheSerLeuAspPheGlyTyrLeuArgAsnGlyCysHisValGluLeuLeuLeu	121 ABGCCCAACCTCAGGATCTTCACCGCGCGCCCTCTACTTCTGAGGACCGCAGG	SULT 15 5.298.29 AF5.298.29 AF5.298.29 CUS Mus musculus clone 2 transgenic Homo sapiens AID (AID) mR CESSION AF5.298.29 REJON AF5.298.29 REJON AF5.298.29 REJON AF5.298.29 AF5.298.29 BUKATYOCKE; MCLEAZOA; Chordata; Craniata; Vertebrata; Eutel BUKATYOCKE; McLeazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri TATHE Somatic hypermutation of the AID transgene in B and non-B JOURNAL Unpublished AUTHORS AU	S aurce urce S s

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Description

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-Q-Cgn2_1/USPTO_spool/US09966880/runat_14062003_175645_16263/app_query.fasta_1.391
-DB-M.Geneseq_101002 -QFWT-fastap -SUFFIX-pin.rng -MINMATCH-0.1 -LOOPCL-0
-LLOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USRR-US09966800_GCGN1_1_263_grunat_14062003_175645_16263 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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1964.298 Million cell updates/sec
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| Sincs/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes human activation-induced cytidine deaminase
(AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and
has cytidine activity similar to APOBEC-1. AID has antiallergic,
antianaemic, antiasthmatic, ophthalmological, anti-HIV and
dermatological activities, and can be used in gene therapp. AID
polymoteotides are useful in methods for identifying drugs for the
treatment of B cell associated immune system disorders, immunodeficiency
diseases and allergies, such as immunoplobulin A (1gA) deficiency
disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic
colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
colitis, asthma, food allergy, drug allergy, rallergic rhinitis, Rosen
immunodeficiency disease, ataxia telahgiectasia, common variable
colitis and IgG subclass selection disorder. The DNA sequences
IgE disorder, and IgG subclass selection disorder. The DNA sequences
cencoding AID may be used for gene therapy and the antibodies to the AID
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 major histocompatibility class II deficiency disease;
auto immunodeficiency syndrome; 1gG subclass selection disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
                                                                         /*tag= a
/product= "activation-induced cytidine deaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2818 BP; 868 A; 548 C; 626 G; 776 T; 0 other;
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198
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Mismatches:
Indels:
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Matches:
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                                                      Location/Qualifiers
30..676
                                                                                                                                                                   99JP-0087192.
99JP-0178999.
99JP-0371382.
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1086.00
100.008
100.008
100.008
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                                                                                                                                                                                                            TOBACCO INC.
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                                                                                                                                                                                                                                                            2000-611715/58.
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Best Local Similarity:
                                                                                                                                                                                                                                                           WPI; 2000-611715,
P-PSDB; AAB24198
                                                                                                     WO200058480-A1
                                                                                                                                                                                                          (NISB ) JAPAN
                                                                                                                                                                                                                     HONJO
                                 Homo sapiens
                                                                                                                                             28-MAR-2000;
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                                                                                                                                                                             24-JUN-1999;
27-DEC-1999;
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200 TCCTITTCACTGGACTTTGGTTATCTTCGCAATAAGAACGGCTGCCACGTGGAATTGCTC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activation-induced cytidine deaminase; AID; cytidine deaminase; antialiergic; antianaemic; antiathmente; cytidine disease; antialiergic; antiasthmente; cytidine anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthme; gdrug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; asthme; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangicatasia; common variable immunodeficiency disorder; anajor histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
                                                                                                                                                  PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly
                                                                                                                                                                                                              AsnProAsnLeuSerLeuArgllePheThrAlaArgLeuTyrPheCysGluAspArgLys
                                                                                                                                                                                                                                     PheLysaspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse activation-induced cytidine deaminase encoding cDNA SEQ ID NO:1.
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/product= "activation-induced cytidine deaminase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC55307 standard; cDNA; 2440 BP
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181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGly 197

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The present sequence encodes mouse activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallargic, and entianaemic, antiasthmatic, ophthalmological, anti-HTV and dermatological activities, and can be used in gene therapy. AID conjuncieotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated IGE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for gene therapy and the antibodies to the AID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu
                                              icleic acid encoding activation induced cytidine deaminase, useful target for drug development for immune-related diseases including
                                                                                                                                                                                                                                                                                                                                                                                                       BP; 706 A; 546 C; 551 G; 636 T; 1 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                       Claim 3; Page 126-130; 174pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.86e-113
1008.00
95.94%
92.89%
WPI; 2000-611715/58.
P-PSDB; AAB24197.
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Best Local Similarity:
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                                             Nucleic acid
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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, antiallergic, and embological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immunos system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergy, allergy allergy, allergy allergy, drug allergy, allergy, allergy chinitis, Rosen immunodeficiency disease, MIC (man)or histocompatibility class) class if deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
                                                                                                                                                                                                                                                                         Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; antiallergic; antianemmic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gentianemmic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gent therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; duty allergy; allergic rhinitis; Rosen disease; DiGeorge disease; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used for gene therapy and the antibodies to the AID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may be used for diagnosis and treatment of these disorders. The sequence represents a genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                     Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including
633 TIGCCCTTGTACGAAGTCGATGACTTGCGAGATGCATTTCGTATGTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6564 BP; 1909 A; 1358 C; 1383 G; 1914 T; 0 other;
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                                                                                                       BP
                                                                                                         DNA; 6564
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99JP-0178999.
99JP-0371382.
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                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honjo T, Muramatsu M;
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                                                                                                       AAC55314 standard;
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present sequenc
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24-JUN-1999;
27-DEC-1999;
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Length:

1.01e-67

Alignment Scores:

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PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys TTCAAAGACTATTTTACTGCTGGAATACATTTGTAGAAAATCGTGAAAGAACTTTCAAA AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglleLeu

AACCCTAACCTCAGCCTGAGGATTTTCACCGCGCGCTCTACTTCTGTGAAGACCGCAAG

393 121 453 141 513 161

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2022 CCTTCCTATTCGGTGACATGACACTTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 2081	2082 ITCATTTACTTCTCATGGCAGTGCCTATTACTTCTTACAATACCCATCTGTCTG	52 52 52 52		2202 CCACCTAGTGGTCCAGGTATTTTCCACAATGTTACATCAACAGGCACTTCTAGCCATTT 2261	52	2262 TCCTTCTCAAAAAGGTGCAAAAAGCAACTTCATAAACACAAATTAAATCTTCGGTGAGGTA 2321	23	GTGTGATGCTGCTTCCTCCCAACTCAGCGCACTTCGTCTTCCTCATTCCACAAAAACCCA	25	535	2442 GCTCTTTTGAGCAAGTTGCTTAGCCTCTGTAACACAAGGACAATAGCTGGAAGCATCC 2501	52	2502 CCAAAGATCATTGCAGGAGACAATGACTAAGGCTACCAGAGCCGCAATAAAAGTCAGTGA 2561	53		63 ArgTyrlleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThr 82 Hill		2682 TCCTGGAGCCCCTGCTACGACTGTGCCCGACATGTGGCCGACATTCTGCGAGGAACCCC 2741	103 AsnLeuSerLeuArgilePheThralaArgLeuTyrPheCysGluAspArgLysAlaGlu 122 1111	123		142 142	2861 AGGIGCGAAAGGGCCTICCGCGCAGGCGCAGTGCAGCAGCCCGCAITCGGGATTGCGATG 2920	142 142	2921 CGGAATGAATGAGTTAGTGGGGAAGCTCGAGGGGAAGAAGTGGGCGGGGATTCTGGTTCA 2980	142 142	2981 CCTCTGGAGCCGAAATTAAAGATTAGAAGCAGAGAAAAGAGTGAATGGCTCAGAGACAAG 3040		3041 GCCCCGAGGAAATGAGAAATGGGGCCAGGGTTGCTTTTTCCCCTCGATTTGGAACCTG 3100	143
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Score: 644.50 Matches: 177 Percent Similarity: 24.02% Conservative: 0 Best Local Similarity: 24.02% Mismatches: 2 Query Match: 59.35% Indels: 560 DB: 21 Gapps: 2			1.1. JArgargGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerphe 42			PACTGGACTTTGGTTATCTTCGCAATAA-GGTATCAATTAAAGTCAGCTTTGCAAGCAG 1241	52	TTTAATGGTCAACTGTGAGTGCTTTTAGAGCCACCTGCTGATGGTATTACTTCCATCCTT 1301	52	TITIGGCALTIGIGICICITATCACATICCTCAAAICCTITITITATTICITITICCAIG 1361	TCCATGCACCCATATTAGACATGCCCCAAAATATGTGATTAATTA	#T 70.TU	TTA 1	52	CCAGCTTTCCTCAGCATCTGAATTGCCTTTGAGATTAATTA	52	1001 1010101010101010101010101010101010	TTAAGCATTTTTGAAAATTAAGGAAGAAGTTTGGGAAAAATTAACGGTGGTTCAATT 1661	ß	CA 1	TTCAACATGGTGATCCCCAGAAAACTCAGAGAAGCCTCGGCTGATGATTAATTA	52	TCTTTCGGCTACCCGAGAGATTACATTTCCAAGACTTCTTCACCAAAATCCAGATGG 1841	52	GTTTACATAAACTTCTGCCCATGGGTATCTCCTCTCTAACACGCTGTGACGTCTGGG 1901	Ŋ	CTIGGTGGAATCTCAGGGAAGCATCCGTGGGGGTGAAGGTCATCGTCTGGCTCGTTGTTT 1961	25	GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 2021	25

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5577 TCCATGCACCCATATTAGACATGGCCCAAAATATGTGATTTAATTCCTCCCCAGTAATGC 6636
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                                                                                                                                                                                                                                                                                            GlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPhe
                   BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 other;
                                                                                                    Conservative:
Mismatches:
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                                                                     Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and carmatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disease, AIDS (auto immunodeficiency syndrome), elevated in deficiency disease, AIDS (auto immunodeficiency syndrome), elevated in deficiency and IgG subclass selection disorder. The DNA sequences
                               immune related disease; allegges allegges antiallarity, opposed disease; antiallarity, antiallarity, antiallarity, antiallarity, antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune System disorder; food allergy, immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy, allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                                         Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.
                                                                                                                    LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeu 181
                                                                                                                                                                                                                                                                                                                                            Activation-induced cytidine deaminase; AID; cytidine deaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 163-170; 174pp; Japanese.
                                                                                                                                                                                                      AAC55339 standard; DNA; 11204 BP
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99JP-0178999.
99JP-0371382.
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24-JUN-1999;
27-DEC-1999;
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අ	7177 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 7236	
ογ	52 52	143
qq	7237 CCTTCCTATTCGGTGACATGACACATTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 7296	8316
ογ	52 52	145
qq	7297 ITCATITACTICTCAIGGCAGIGCCIATIACTICTTIACAAIACCCAICIGICIGCTII 7356	83/6 TTTTACTGCTGGAATACTTTTGTAGAAACCACGAAAGAACTTTCAAAGCCT
οχ	52 52	165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeuLeu
qu	7357 ACCAAAATCTATTTCCCCTTTTCAGATCCTCCCAAATGGTCCTCATAAACTGTCCTGCCT 7416	8436
οy	52 52	
qq	7417 CCACCTAGTGGTCCAGGTATATTTCCACAATGTTACATCAACAGGCACTTCTAGCCATTT 7476	ID AAC5531/ Standard; DNA; 2/1 BP. XX
ογ	52 52	AAC55317;
QO	7477 TCCTTCTCAAAAAGGTGCAAAAAGGAACTTCATAAACACAAATTAAATCTTCGGTGAGGTA 7536	
ογ	52 52	
qq	7537 GIGIGAIGCIGCIICCICCCAACICAGCGCACIICGICTICCICAIICCACAAAAACCCA 7596	KW Activation-induced cytidine deaminase; AID; cytidine deaminase; KW immune related disease; allergy; allergic disease; antiallergic;
οy	52 52	
qq	7597 TAGCCTTCCTTCACTCTGCAGGACTAGTGCTGCCAAGGGTTCAGCTCTACCTAC	
δy	52 52	
qa	7657 GCTCTTTTGAGCAAGTTGCTTAGCCTCTGTAACACAAGGACAATAGCTGCAAGCATCC 7716	
δ	52 52	XX OS Homo sapiens.
q	7717 CCAAAGATCATTGCAGGAGACAATGACTAAGGCTACCAGAGCCGGAATAAAAGTCAGTGA 7776	XX PN W0200058480-A1.
Qy		XX PD 05-OCT-2000.
qa		XX PF 28-MAR-2000; 2000WO-JP01918.
ςς Q	63 ArgTyrileSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThr 82 	XX PR 29-MAR-1999; 99JP-0087192. PR 24-JUN-1999; 99JP-0371382. PR 27-DEC-1999; 99JP-0371382.
Qy		(NISB) JAPAN
qq		OCNOH (/CNOH)
δλ	103 AsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLysAlaGlu 122	PI Honjo T, Muramatsu M; XX
q		DR WPI; 2000-611715/58. xx
ογ		PT Nucleic acid encoding activation induced cytidine deaminase, useful PT a target for drug development for immune-related diseases including PT allergies -
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δ	142	Etho water the transfer of E
q	8076 AGGIGCGAAAGGGCCTICCGCGCAGGCGCAGTGCAGCAGCCCGCATICGGGATTGCGATG 8135	
δλ	142	
ф	8136 CGGAATGAATGAGTTAGTGGGGAAGCTCGAGGGGAAGAAGTGGGGGGGG	
δλ	142 142	
QQ	8196 CCTCTGGAGCCGAAATTAAAGATTAGAAGCAGAGAAAAGGGTGAATGGCTCAGAGACAAG 8255	CC disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, altergic CC colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen
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II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated 1gE disorder, and IgG subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents the exon 3 genomic DNA sequence of human AID.
                                                                                                                     72
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                                                                                                                                                                       ed protein; cDNA library; clone; transmembrane protein; sequence cloning; hybridization cloning; gene therapy;
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                                       G; 53 T; 0 other;
                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                        Polynucleotide sequence of the lp547_4 clone.
                                                                                                                                                                                                                                 GlyValGlnIleAlaIleMetThrPheLys 142
                                                                                          Gaps:
                                                                                                      US-09-966-880A-8 (1-198) x AAC55317 (1-271)
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/product= lp547_4
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                                       Sequence 271 BP; 47 A; 95 C; 76
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17-FEB-1999;
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This is the polynucleotide sequence of the clone 1p547_4, which was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins, or by identification as a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.

The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, hemostatic immune stimulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chinhibin activity, chemotactic/chemokinetic activity, and thrombolytic activity, chemotactic/chemokinetic activity, and thunor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection of bodily characteristics such as, eg. weight, color, skin, etc., effecting biorhythms or circadian cycles; enhancing fertility; treatment
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      Merberg
                                                                                                                                                                                 encoding human secreted proteins used for
McCoy JM, LaVallie ER, Collins-Racie LA,
Agostino MJ, Steininger RJ;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                        Claim 16; Page 104; 125pp; English.
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996 ---GATGATCAAGGAAGATGTCAGGAGGGGCTGCGCACCCTGGCCGAGGCTGGGGCCAAA 1052

CysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGln 135

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ABA90962;
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|1053 ATTCAATAATGACATGAGTGAATTTAAGGACTGCTGGGACACCTTTGTGGACCACCAG 1112
                                                                            1113 GGATGTCCCTTCCAGCCCTGGGATGGACTAGATGAGCACAGCCAAGACCTGAGTGGGAGG 1172
 IleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHis 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of immunodeficency (SCID), autoimmune disorders e.g. severe combined systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders e.g. multiple sclerosis, andiammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation
                                                                                                                                                                                                                                                                                                                      Human; secreted protein; ss; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; vasotropic; neuroprotective; virucide; antiinfermility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; lumune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; periodontal disease; osteoporosis; osteoarthritis; latheimer; sdisease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                        156 GluArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
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Wong GG;
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Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                               Human cDNA encoding a secreted protein lp547_4.
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                                                                                                                                                                                                      AAS59293 standard; cDNA; 1534 BP.
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Treacy M, Agostino MJ, Steininge
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Clark H, Fechtel K, Merberg D;
                                                                                                                                               1173 CTGCGGCCATTCTC 1187
                                                                                                                   176 LeuArgArglleLeu 180
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04-DEC-2000; 2000US-0729674.
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P-PSDB; AAU39075.
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graft-versus-host diseases (GVHD), in the induction of tumour immunity, in the treatment of burns, incisions and ulcers; as well as in treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, alzahimaris, Parthinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and SNy-Drager syndrome, infections, inflammatory bowel disease, ulcers, bone respensable or stroke, sepsis, inflammatory bowel disease, ulcers, bone respensable on the ability of inhibins to decrease fertility in femals and decrease spermatogenesis in male mammals. The female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArg 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPheSerLeuAsp 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 GluargThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerargGln 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 TyrargvalThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAla
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 1534 BP; 495 A; 363 C; 345 G; 331 T; 0 other;
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83
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59
12
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Mismatches:
Indels:
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Matches:
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61.62%
44.86%
35.91%
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Best Local Similarity:
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naematopoiesis regulators, tissue growth modulators and/or cadherin
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                                              Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; limmune disorder; bacterial infection; fungal infection; cancer; tumour; autoimnune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophila, cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New secreted proteins and encoding polynucleotides, useful in gene
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Steininger RJ, Spaulding
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Merberg D, Treacy M, Agostino MJ,
Wong GG, Clark H, Fechtel K;
                          NO 173.
                          Human polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                               97US-067454P
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LAVALLIE E R.
COLLINS-RACIE L A.
 (first entry)
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STEININGER R J.
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14-FEB-2002
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1113 GGATGTCCCTTCCAGCCCTGGGATGGACTAGATGAGCACCAGAGCCAAGACCTGAGTGGGAGG 1172
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suppressors. The polypeptides and polynucleotides are useful in gene therapies, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial or fungal infections, autoimmune disorders, cancer, systemic lupus erythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or osteoarthritis; central and peripheral nervous system diseases and neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome; haemophilia, cardiac infarction or stroke, inflammations, shock, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthritis, inflammatory bowel disease or conforts of sisease, or tumours or cancers, pemphigus vulgaris or pemphigus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1534 BP; 495 A; 363 C; 345 G; 331 T; 0 other;
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Mismatches:
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                                                                                                                                                                     1050 CATGCAGAGCTGTGCTTCCTGGACGTGATTCCCTTTTGGAAGCTGGACCTGGACCAGGAC 1109
                                                                                                                                                                                                                                                                                                                                                                                  115
116 CysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGln 135
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                                                      55
                                                                                                                                56 HisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCys
                                                                                                                                                                                                                              1110 TACAGGGTTACCTGCTTCACCTCCTGGAGCCCCTGCTTCAGCTGTGCCCAGGAAATGGCT
                                                                                                                                                                                                                                                                                     96 AspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPhe
                                                                                                                                                                                                                                                                                                        136 IlealallemetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1284 ATTTCAATACTGACATACAGTGAATTTAAGCACTGCTGGGACACCTTTGTGGACCACCAG
                                                      --AsnGlyCys
                                                                                                                                                                                                          76 TyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RNA editing enzyme and poly:nucleotide(s) encoding it - useful for recombinant production of the enzyme and treatment and detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; human; RNA editing enzyme; REE; pharmaceutical carrier; c
viral disease; circulatory system disorder; RNA processing;
hypercholesterolaemia; alpha-galactosidase; apolipoprotein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a /product= "RNA editing enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human RNA editing enzyme nucleotide sequence.
                                                      ----PheGlyTyrLeuArgAsnLys----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1404 CTGCGGGGCATTCTG 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 LeuArgArgIleLeu 180
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P-PSDB; AAW77092.
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                                                        46
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                                                                                     Human; RNA-associated protein; cell proliferation; cancer; inflammation; limmune response; reproductive disorder; actinic keratosis; atherosclerosis; arteriosclerosis; burstits; cirrhosis; hepatitis; mixed connective tissue disease; myelofibrosis; primary thrombocythemia; paroxysomal nocturnal hemoglobinuria; polycythermia vera; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPheSerLeuAsp 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hemoglobinuria, polycythermia vera, psoriasis, primary thrombocythemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human RNA-associated protein. The expression of RNA-associated proteins is closely associated with reproductive tissues, nervous tissues, cell proliferation including cancer, inflammation and immune responses, and so they may be used for diagnosis, treatment or prevention of cell proliferative, immune/inflammatory disorders, and reproductive disorders. Diseases and disorders which may be treated include actinic keratosis, atherosclerosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysomal nocturnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides and polynucleotides, useful for preventing and treating a disorder associated with increased or decreased expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guegler KJ, Gorgone GA, Patterson R, Lal P, Azimzai Y, Yue H, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1446 BP; 370 A; 374 C; 393 G; 308 T; 1 other;
                                                                                                                                                                                                                                                           Location/Qualifiers
32..146
/*tag= a /product= "RNA-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                    cDNA encoding a human RNA-associated protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 119; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0156039.
98US-0158720.
98US-0186815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA associated proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.86e-37
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61.628
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               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCY - ) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and cancers, and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley NC,
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Best Local Similarity:
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22-SEP-1998;
04-NOV-1998;
08-APR-1999;
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                 25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                                                                                                                     trauma; ss
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                                                The human RNA editing enzyme (REE) is used in a pharmaceutical carrier for the treatment of cancer, viral diseases and circulatory system disorders. The enzyme is used in vivo for the correct processing of RNA transcripts of genes e.g. change of a codon in apolipoprotein B (apoB) RNA to give a 100 and 48 kDa product transcribed from the same gene. Certain disorders have been linked to incorrect RNA editing, e.g. failure of apo B editing leads to excessive apoB 100 production and hypercholesterolaemia. Other disorders thought to be linked to incorrect RNA processing include aberrant alpha-galactosidase processing in Fabry's disease and neurofibromatosis type I. The enzyme can be produced recombinantly to treat related disorders. It can also be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342
                                                                                                                                                                                                                                                                                                                                                                                                          TTCTACTTCCAATTTAAAAACCTATGGGAAGCCAACGATCGGAACGAAACTTGGCTGTGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                223 TICTGCGACGACATACTGTCTCCTAACACAAGTACCAGGTCACCTGGTACACATCTTGG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 AATCTCACCATCTTCACCGCCTCTACTACTTCCAG---TATCCATGTTACCAGGAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCTTGGAAGGGA 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuArgllePheThrAlaArgLeuTyrPheCysGluAspArgLysAlaGluProGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
                                                                                                                                                                                                                                                                                                                                                                                 PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys 30
                                                                                                                                                                                                                                                                                                                                                                                                                                31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThrSerTrp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuArgAsn------LysAsnGlyCysHisValGluLeuLeuPheLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 GGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATCATGGACTATGAAGATTTT
                                                                                                                                                                          recombinantly to treat related disorders. It can also be used antibodies for immuno-based detection of REE expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| TTAAAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGAGTCTC
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of disorders associated with incorrect RNA processing
                                                                                                                                                                                                                            Sequence 610 BP; 158 A; 154 C; 154 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                  610
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Matches:
Conservative:
Mismatches:
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                          Fig 1; 27pp; English
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369.50
58.52%
44.89%
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                          Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the cDNA encoding human RNA editing enzyme REE-2. CMDA encoding REE-2 was initially isolated in a prostate tumnour cDNA library, with the present sequence representing a consensus. REE-2 has chemical and structural homology with the human apoB mRNA editing protein HEBPR (28% identity), the rat HEBPR homologue REBPR (30% identity), and a portion of the mRNA editing enzyme phorbolin I (43% identity). REE-2 was found to be expressed in a variety of cDNA libraries, a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis, treatment and prevention of such diseases via the modulation of transcript editing, which in turn has effects on the encoded protein (e.g., an alteration in protein activity). The invention specifically relates to methods of detecting nucleic acids encoding human REE-2 in a
                                                                              phorbolin I homologue, cancer; tumour; autoimmune disorder;
circulatory system disorder; hypercholesterolaemia; viral infection;
neurological disease; neurofibromatosis; transcript editing; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting polynucleotide encoding human RNA editing enzyme comprising hybridizing an isolated and purified polynucleotide complementary to the polynucleotide and detecting the hybridization complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proportion of which were derived from tumours, neuronal tissues, immaysystem cells or synovial tissue from arthritis patients. REE-2 is therefore thought to be associated with the development of cancer, autoimmune disorders, circulatory system disorders (e.g. hypercholesterolaemia), viral infections and neurological diseases neurofibromatosis). REE-2 or its nucleic acids may be used in the
                                                   REPR homologue;
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9
                                                   enzyme; REE-2; human; nerk nomologue; cancer; tumour; autoimmune homologue; cancer; tumour; autoimmune
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Indels:
encoding human RNA editing enzyme REE-2.
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                                                                                                                                                                                                                                                                                                                                                                     "Human REE-2"
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phorbolin I
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2000US-0225267
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08-NOV-2000;
            11) | 11 | 11| | 123 TTCTGGGACGACATACTGCTACCAAGTACCAGGTCACCTGGTACACATGTTGG 282
                                                                                                                                                           GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr 144
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                                          LeuArgAsn------LysAsnGlyCysHisValGluLeuLeuPheLeuArgTyr
                                                              163 TTCCGAAACCAGGTGGATTCTGAGACCCATTGTCATGCAGAAAGGTGCTTCCTCTGGG
                                                                                                65 IleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThrSerTrp
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
                                              enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                       31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
   (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent CDNA sequences encoding for the novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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2000US-0249244.
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P-PSDB; AAU23550.
08 - NOV - 2000;
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441 AATCTCACCATCTTCACCGCCCGCCTCTACTACTTCCAG----TATCCATGTTACCAGGAG 497
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                                 125 GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr
                                                                                                   145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly
                                                                                                                                    558 AAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCTTGGAAGGGA
                                                                  498 GGGCTCCGCAGCCTGAGTCAGGAAGGGGTCGCTGTGGAGATTTT
                                                                                                                                                                      165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
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                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding novel human enzyme polypeptide #623.
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2000US-0218290.
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2000US-0224519
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, valnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
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                                                                                                                                                                                                                                                                                                  Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer
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P-PSDB; AAB57061.
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Homo sapiens.
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2000US-0232081.
2000US-0231968.
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2000US-0230437.
2000US-0230438.
2000US-0231242.
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Ruben SM;
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P-PSDB; AAU23537.
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11-DEC-2000;
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preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous Novel polypeptides and polynucleotides useful for diagnosing diseases

Claim 4; SEQ ID No 633; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. althma), cardiovascular disorders (e.g. althmancry disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. aherosclerosis), colynucleotides of the invention can also be used in gene therapy. Ass40785-AaS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention can also be used in gene therapy. Ass40785-AaS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.

CC Ass40785-AaS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.

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other; Sequence 987 BP; 231 A; 298 C; 232 G; 224 T; 2

Alignment Scores:			
Pred. No.:	3.04e-35	Length:	.86
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Percent Similarity:	58.52%	Conservative:	24
Best Local Similarity:	44.898	Mismatches:	64
Query Match:	34.02%	Indels:	6
DB:	22	Gaps:	4

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Liu C,
Wang Z,
Zhou P,
         (HYSE-) HYSEQ INC.
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                                      PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys 30
                                                                                                          31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyr 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous localised neuropathies and central nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, ch. S. disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      917 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG-----GGCGTC 864
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                Wang D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 TyrValValLys-----ArgArgAspSerAlaThrSerPheSerLeuAspPheClyTyr
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              Ren F, W
Zhang J;
           Qian XB,
Yang Y,
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Mismatches:
    tu C, Xue AJ,
Drmanac RT;
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Matches:
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                                                                                                                                                    Novel nucleic acids and polypeptides, us
such as central nervous system injuries
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    Chen R,
Xu C, )
Asundi V, Che
Wehrman T, Xu
Goodrich R,
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369.50
58.52%
44.89%
34.02%
                                                                                      2001-442253/47.
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566 AAATATTGTTGGGAAAACTTTGTGTACAATGATAATGAGCCATTCAAGCCTTGGAAGGGA 507

상 임 QΩ

Search completed: June 19, 2003, 17:58:08 Job time: 233 secs

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OW protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2003, 13:52:31; Search time 1384 Seconds

(without alignments)
2316.984 Million cell updates/sec

Title: US-09-966-880A-8
Perfect score: U86
Sequence: Napape 10.0 / Yapapext 0.5
Yapape 10.0 / Yapapext 0.5
Whinimum bs seq length: 0.0
Waximum watch 0.8
Histing first 45 summaries
Command line parameters:
Waximum watch 0.8
Listing first 45 summaries
Command line parameters:
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-0-Cqu2_1/USFPO_spool_VUS9986880/runat_14062003_175645_16282.Pummad.0.-USFPU_FANT=0.0-THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -THR_MAX=100 -USFPU_FANT=0.0-VORD=0.-LANGOUGLEGO
-USFRU-PANCORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VORD=0.0-VOR
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

[ES] Description		BG686133 602638412	AL559877 AL559877	BG758510 602712721	BO055935 AGENCOURT	BG757089 602715124																															BG744603 602722683	SINTS		linear EST 01-MAY-	CDNA CIONE IMAGE:4/06234 3				Craniata; Vertebrata; Euteleostomi; Catarrhini: Hominidae: Homo		Mammalian Gene Collection (MGC)
SUMMARIES		368613					BG/57392 BF975166	AJ446140	AJ453647	AJ450296	AJ430317 RG144705	BF238155	AJ449745	BG686876	AJ450295	BE973096	BI834760	BQ877348	BM914942	BE886229	BG025943	BG032405	BQ/0//23 BM474553	BM424095	BM809617	BM917194	BC021080	BC009683	BE882870	BM473129	BQ056030	BQ058970	BQ061901	BM935138	BQ052514	BO065295	BG744603	ALIGNMENT		74:	ошон я		30		Chordata; C	nib any	Health,
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em_gss_other:*

em_gss_fun:* em_gss_mam:* em_gss_mus:*

em_gss_inv:* em_gss_pln:*

em_gss_hum:*

db_gss:*

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gb_est3: *
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em_estfun: *

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em_estro:*
em_htc:*
gb_estl:*

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em_esthum:*
em_estin:*
em_estmu:*
em_estov:*

EST:*

Database :

em_gss_pro:* em_gss_rod:*

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AL559877 LTI_FL011_BC1 Homo sapiens cDNA clone CSODG003YB14 5 prime
                                   **Mote--Vector: pcMvSpORT 6: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco Rv sites of the pcMvSpORT 6 vector. Feng Library was constructed by Life Technologies. Contact: 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 G10 8371 Email: fliang@lifetech.com URL: 217 c 202 g 226 t 2 others
                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 865)
S Li,WB., Gruber,C., Jessee,J. and Polayes,D.
L Unpublished (2001)
L Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="B cells from Burkitt lymphoma"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                              , mRNA sequence.
AL559877
AL559877.1 GI:12905793
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KEYWORDS
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                                                                                                                                                                                                                                   /clone="Indage:4/66234"
/clone="Indage:4/66234"
/tissue_type="primary B-cells from tonsils (cell line)"
/tab_host="Brimary B-cells from tonsils (cell line)"
/tab_host="Brimary B-cells; vector: porB7; Site_1: XhoI;
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Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size=selected >500bp
for average insert size 1.8kb. Library constructed by Ling
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
             Contect: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Email: gapbs-r@mail.nih.gov
Tissue Prourement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
http://image.lhn.gov
Plate: LLCMIG26 row: g column: 03
High quality sequence stop: 740.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                            /organism="Homo sapiens"
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JOURNAL
COMMENT
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Alignment Scores: 9.51e-131 Length: 872 Pred. No.: 1086.00 Matches: 198 Score: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 12.00 Mismatches: 0 DB: 12.00 Mismatches: 0 US-09-966-880A-8 (1-198) x BG758510 (1-872)	Oy 1 MetaspSerLeuLeuMetasnargargLysPheLeuTyrGlnPheLysasnValargTrp 20	Qy 21 AlaLysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr 40 	Oy 41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60	Oy 61 PheLeuargTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrargValThrTrp 80	Qy 81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100 Db 1	Db 366 AACCCCAACCTCAGGATCTTCACCGCGCGCCTCTACTTCTGTGAGGACCGCAAG 425 Qy 121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIIeMetThr 140	Qy 141 PhelysaspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160 	Qy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180	Oy 181 LeuProLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198 	RESULT 4 BQ065440 LOCUS BQ065440 DEFINITION AGENCORE_6855061 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929977	_	REFERENCE 1 (bases 1 to 953) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Email: cgapbarfwall.nih.gov Tissue Procurement: Lou Standt CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation
11	Qy 121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 140	Qy 141 PheLysaspTyrPheTyrCysTrpasnThrPheValGluasnHisGluargThrPheLys 160 	Oy 161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180 	Oy 181 LeuProLeuTyrGluValAspAspLeuargAspAlaPheArgThrLeuGlyLeu 198 	RESULT 3 BG758510 LOCUS LOCUS BG758510	l GI:14069 ens ; Metazoa;	theria; Primates; to 872) >://mgc.nci.nih.go %titutes of Health	оошн	CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through that I M. A. C. P. Consortium I M. a.t.	http://image.llni.gov Plate: LLCM1698 row: i column: 06 High quality sequence stop: 836. Location/Qualifiers		Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." BASE COUNT 211 a 221 c 212 g 228 t

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604 TTGCCCCTGTATGAGGTTGATGACTTACGAGACGCATTTCGTACTTTGGGACTT 657
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9
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TITLE
JOURNAL
COMMENT
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/clone=lib="NIH_MGC_9977"
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Plate: LLCM2108 row: p column: 10
High quality sequence stop: 634.
Location/Qualifiers
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                                                                                       /organism="Homo sapiens"
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BQ055935 1052 bp mRNA 11near EST 29-MAR-2002
AGENCOURT_6796291 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808181
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Alignment Scores: 1.17e-127 Pred. No.: 1.62.00 Matches: 193 Percent Similarity: 100.00% Best Local Similarity: 100.00% Mismatches: 0 Query Match: 12 Gaps: 0 Use-09-966-880A-8 (1-198) x BG757089 (1-820)	1 MetaspSerLeuLeuMetasnargargLysPheLeuTyrGlnPheLysAsnValargTrp 20	21 AlalysGlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThr 40 	41 SerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCysHisValGluLeuLeu 60 	61 PheLeuargTyrlleSeraspTrpAspLeuaspProGlyargCysTyrArgValThrTrp 80 	81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100	ASSET OF STREET OF THE STREET OF THE STREET	121 AlaGlubroGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 140 	141 PhelysAspTyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLys 160 	161 AlaTrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglleLeu 180 	181 LeuProteuTyrGluValAspAspLeuArgAspAlaPhe 193 	N.	_	FENCE 1 (bases 1 to 693) HORS NIH-MGC http://mgc.nci.nih.gov/. HORS NIH-MGC http://mgc.nci.nih.gov/. RNAL National Institutes of Health, Mammalian Gene Collection (MGC) RNAL Uppublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Labbratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
Alignment Pred. No.: Score: Percent Si Best Local Query Matc DB: US-09-966-	Qy	Qy Dp	Qy	Qy Db	oy Db	da da	Oy Dp	Oy Dp	Qy Dp	oy Op	RESULT 7 BG757392 LOCUS DEFINITIC	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE TUTHORS TITLE JOURNAL COMMENT
244 TTCCTCCGCTACATCTCGGACTGGGACCTAGACCCTGGCCGCTGCTACCGCGTCACCTGG 303 81 PheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgGly 100	121 AlaGluProGluGlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThr 140 	141 PhelysasptyrPheTyrCysTrpasoThrPheValGluasnHisGluargThrPheLys 160 	161 AlatrpGluGlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180 	181 LeuproLeuTyrGluValAspAspLeuArgAspAlaPheArgThrLeuGlyLeu 198 		BG757089 BG757089.1 GI:1406774 EST.	C H B M	H 01 -	Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:			Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/NboI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). COUNT 210 a 230 c 200 g 180 t
0 dy 0 dy 0 dy 0 dy 0 dy	Oy Dp	cy eg	oy D	Oy Db	RESULT 6 BG757089 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE TOURNAL	COMMENT		FEATURES	ň .	BASE CC

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TITLE
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Site_2: EcoRI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: aGCAGGGGG(G). Size-selected >500bp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald Mr. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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BF975166 942 bp mRNA 11near EST 22-JAN-2001
602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
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                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov

Plate: LLCM1207 row: a column: 16

High quality sequence stop: 707.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                      mRNA sequence.
BF975166
BF975166.1 GI:12342381
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Best Local Similarity:
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		9 OZ 61 E1	AUTHORS Buerstedde, J.M. TITLE Gallus gallus bursal lymphocyte EST JOURNAL Unpublished (2002) COMMENT Contact: Buerstedde JM Callular Immunology Heinrich-Pette-Institute Martinistr: 52, 20251 Hamburg, Germany Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.	/cr /cr /cr /ce /ce /ce /de /de	Alignment Scores: 1.11e-116 Length: 696 Score: 977.00 Matches: 177 Percent Similarity: 93.94 Conservative: 9 Best Local Similarity: 89.394 Mismatches: 12
0y 90 pPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArgG1 100 1111111111111111111111111111111	AJ446140 LOCUS AJ446140 LOCUS DEFINITION AJ446140 AJ446140 AJ44640 AJ46440 AJ4	REFERENCE 1 (bases 1 to 757) AUTHORS Buerstedde,J.M. TITLE Gallus gallus bursal lymphocyte EST JOURNAL Unpublished (2002) COMMENT Contact: Buerstedde JM Callular Immunology Hainrich-Pette-Institute Martinistr. 52, 20251 Hamburg, Germany Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html. FEATURES 1. 757	/organism="Gallus gallus" //db_xref="Laxon:9031" //clone="12/911" //clone="12/91" //clone="12/	Alignment Scores: Pred. No.: Pred. No.:	Oy 1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp 20

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AJ450317 rikenl Gallus gallus cDNA clone 24n22rl, mRNA sequence. AJ450317.1 GI:20217538
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 688)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
                                                                                                                                                        PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsnH1sGluArgThrPheLys
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Mismatches:
Indels:
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Matches:
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199 c 187 g 170 t
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                                                              6.77e-108
910.00
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Best Local Similarity:
Query Match:
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Achosaunia; Aves: Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 729)
Buerstedde,J.M.
                                                                               MetaspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
                                                                                                                                                     61 PheLeuargTyrIleSeraspTrpAspLeuAspProGlyArgCysTyrArgValThrTrp
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Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
1. 729
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Query Match:
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361 GAATACATTIGTAGAAAATCGTGAAAGAACTTTCAAAGCCTGGGAAGGGCTACATGAAAA 420
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 522)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1077801
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Gaps:
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Location/Qualifiers
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         Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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1. .688
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/191 c 178 g 156 t
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Matches:
Conservative:
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AJ449745 AJ449745 rikenl Gallus gallus cDNA clone 23a2rl, mRNA sequence.
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                                                                                                         101 AsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArgLys
                                                                                                                                                              1 MetAspSerLeuLeuMetAsnArgArgLysPheLeuTyrGlnPheLysAsnValArgTrp
                                                                                                                                                                                                                                                     141 PheLysAspTyrPheTyrCysTrpAsnThrPheValGluAsn 154
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/dev_stage="2-3 weeks old"
/note="CB inbred strain"
182 c 167 g 151 t
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="23a2r1"
/clone="lib="riken1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_ivpe="primary B-cells from tonsils (cell line)"
/lab.host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: Xhol;
Site_2: EccRit: CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Geraid M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH,MGC Library."
                                                                                                         BF238155
601811880F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054915 5',
TICTGICCGGCTAACCAGACAACTICGGCGCAICCTITTGCCCTTGTACGAAGTCGATGA 480
                                                                                                                                                                                                                                              E I (Dasses 1 to 341)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.lnl.gov
Plate: LiCM895 row: p column: 20

High quality sequence stop: 541.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 541)
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Matches:
Conservative:
Mismatches:
                                        188 pLeuargaspalaPheargThrLeuGly 197
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/clone="IMAGE:4054915"
/clone_lib="NIH MGC_48"
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us-09-966-880a-8.p2n.rst

360 TTCACCTCGGGAGCCCCGGTTATGACTGTGCCCGACATGTGGCTGACTTCCTTC
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Search completed: June 19, 2003, 19:02:59 Job time: 1389 secs

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Perfect score:

Run on:

Sednence:

Scoring table:

Searched:

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Sequence 24, Appl
Patent No. 5180808
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US-09-210-228-11
US-09-210-288-11
US-08-487-8288-13
US-08-998-416-977
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US-08-552-1369-1
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US-08-080-255-4
US-08-465-713-4
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US-08-061-376-4
US-08-320-559-1
US-08-327-392-1
US-08-306-691B-55
US-08-545-860D-1
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APPLICANT: Bandman, olga
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
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US-09-103-840A-1
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MEDIUM TYPE: Diskette
COMPUTER: DISKET
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PCT-US93-06251-10
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STREET: 3174 Porter Drive
CITY: Palo Alto
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Sequence 2, Application US/08816241
Patent No. 5804185; GENERAL INFORMATION:
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
     08877999999999
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-Q-cgn2_1/USPTO_spool/US09966880/runat_14062003_175646_16331/app_query.fasta_1.391
-De-lssued_parents_1.M. -QPRT-fastap - SUFFIX-PDA.rni -MINMATCH=0.1. -LOOPCL=0
-LISSUEQ_Parents_1.M. -QPRT-fastap - SUFFIX-PDA.rni -MINMATCH=0.1. -LOOPCL=0
-LIST-45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX-100 - THR_MIN=0 - ALIGN=15
-MODE-LOOPL
-USPR-USO9966880_GCGN_1_1_40_erunat_14062003_1755646_16331 - NCPU=6 - ICPU=3
-NO_MMAP - LARGEQUERY - NG_SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THRRADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 123, Appli
Sequence 123, Appli
Sequence 16, Appli
Sequence 16, Appli
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Sequence 2, Appli
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1190.627 Million cell updates/sec
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1086
1 MDSLIANNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL
                                                                                                                                                                                       June 19, 2003, 17:42:06; Search time 51 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcyu(5_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcyu(5_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
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US-09-128-395-2
US-09-687-895-2
US-09-040-482-2
US-08-158-682A-3
US-08-158-682A-1
US-08-15-203-1
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US-09-049-698-16
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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77.5
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Score

Result

110

Jatabase :

54, Appl 1, Appli 1, Appli

4, Appli 4, Appli 4, Appli 1, Appli 1, Appli 1, Appli 1, Appli 11, Appli 11,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 AAATATTGTTGGGAAAACTTTGTGTACAATGATGAGCCATTCAAGCCTTGGAAGGGA 519
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APPLICANT: GOli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                      US-09-966-880A-8 (1-198) x US-08-816-241-2 (1-610)
                                                                                                                                        Length:
Matches:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
                                                                                                                                   6.02e-38
369.50
58.52%
44.89%
SEQUENCE CHARACTERISTICS:
LENGTH: 610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                         LIBRARY: PROSTUT09
CLONE: 1646833
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                               IMMEDIATE SOURCE:
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STATE:
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145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 TTCTGCGACGACATACTGTCTCCTAACACAAAGTACCAGGTCACCTGGTACACATCTTGG
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Mismatches:
                                   SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF-0239 US TELECOMMUNICATION INFORMATION: TELEPHATION: 415-845-4166 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 610 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                     APPLICATION NUMBER: US/09/128,395
FILING DATE:
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
                                                                                                                                                                                                               NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.02e-38
369.50
58.52%
44.89%
34.02%
              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                CURRENT APPLICATION DATA:
Diskette
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HMEDIATE SOURCE:
LIBRARY: PROSTUT
CLONE: 1646833
US-09-128-395-2
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Best Local Similarity:
Query Match:
MEDIUM TYPE:
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                                                 SOFTWARE:
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 110 ThralaArgLeuTyrPheCysGluAspArgLysAlaGluProGlu------GlyLeu 126
                                                                                                                127 ArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyr 146
                                                                                                                                                                                    147 CysTrpAsnThrPheValGluAsnHisGlu-----ArgThrPheLysAlaTrpGlu 163
                                                                                                                                                                                                     164 GlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIle 179
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
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STREET: 3174 Porter Drive
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FRS4SEQ VERSION 1.5
SOFTWART APPLICATION DATA:
APPLICATION NUMBER: US/09/040,482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/687,895
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09040482 Patent No. 5916556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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50.00%
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STRANDEDNESS: single
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MEDIUM TYPE: Diskett
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Best Local Similarity:
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520 TTAAAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGAGTCTC 567
                                                                                                             APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN MRNA EDITING ENZYME NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                           STREE: CA Alto
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                                                                                                                                                                                                                                                                                                                                                                               SCENAIR SISTEMENT SOFTWARE: FEASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
PELLING DATE: FILE HEREWITH
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
RECISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                Sequence 2, Application US/08687895
Patent No. 5747319
GENERAL INFORMATION:
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271.00
50.00%
35.80%
24.95%
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                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LIBRARY: MUSCNOT1
CLONE: 57953
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Best Local Similarity:
Query Match:
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                                             US-08-687-895-2
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                                RESULT
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                                             PheLeuTyrGlnPheLysAsnValArgTrpAlaLysGlyArgArgGluThrTyrLeuCys
                                                                                                               31 TyrValValLysArgArgAspSerAlaThrSerPheSerLeuAspPheGlyTyrLeuArg
                                                                                                                                                  366 TATGTGGTTGAAGCACAGGGCAAGGGGGCCAAGTGCAGGCATCTCGGGGATACCTAGAG
                                                                                                                                                                                    AsnLysAsn---GlyCysHisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAsp
                                                                                                                                                                                                                                                      70 LeuaspProGlyArgCysTyrArgValThrTrpPheThrSerTrpSerProCysTyrAsp
                                                                                                                                                                                                                                                                          110 ThrAlaArgLeuTyrPheCysGluAspArgLysAlaGluProGlu-----GlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                   818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 GlyLeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArglle 179
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TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE & DURKEE
STREET: 321 No. 5434058th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771 GACATTCAGGAGAACTTCCTATACTACGAGGAGAAGTTGGCAGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/158,682A
         US-09-966-880A-8 (1-198) x US-09-040-482-2 (1-891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD:085
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08158682A Patent No. 5434058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 GATCAACAA---AATCGGCAAGGTCTCAGGGACCTTGTTAACAGTGGAGTAACTATTCAG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 ValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08158682A
Patent No. 5434058
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrSerPheSerLeuAspPheGlyTyrLeuArgAsnLysAsnGlyCys-
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43
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: 321 No. 5434058th Clark Street, Sulte
                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                        24 ArgArgGluThrTyrLeuCysTyrValValLys----
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                                                                                                                                                                                                         Length:
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                                                                        DNA (genomic)
                                                                                                                                                                                                      2.15e-17
210.00
56.30%
35.56%
19.34%
879 base pairs
                                     single
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FILING DATE:
CLASSIFICATION: 435
                 nucleic acid
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STATE: Illinois
COUNTRY: USA
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Best Local Similarity:
Query Match:
                                   STRANDEDNESS:
TOPOLOGY: lin
                                                                        MOLECULE TYPE:
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                                                                                                             NAME/KEY:
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US-08-158-682A-3
                                                                                                                                                                                    Alignment Scores:
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137 CGGAAAGAGACCTGTCTGCTGTATGAGATCAACTGGGGAGGAAGGCACAGCATCTGGCGA 196
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56
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61
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               E: ARNOLD, WHITE & DURKEE
321 No. 5550034th Clark Street, Suite 800
                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 19930209
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 ArgArgGluThrTyrLeuCysTyrValValLys ----
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                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2/100/
REFERENCE/DOCKET NUMBER: 180:069
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 879 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.01e-16
201.00
47.65%
32.94%
18.51%
 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                               CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                60610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-015-203-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 CACGTTGAAGTCAATTTCATAGAAAATTTACTACAGAAAGATACTTTTGTCCAAACACC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518 TCCCCTTCGAATGAAGCTCATTGGCCAAGGTACCCCCATCTGTGGGTGAGGCTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08015203
Patent No. 5550034
GENERAL INFORMATION:
APPLICANT: Teng, BaBie
APPLICANT: Davidson, Nicholas O.
APPLICANT: Burant, Charles F.
TITLE OF INVENTION: Apolipoprotein B RNA Editing Protein:
TITLE OF INVENTION: Composition and Method
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                     879
256
21
61
28
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                 ARCD: 085
            NAME: COOLLEY, Ronald B.
REGISTRATION UNUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            LENGTH: 879 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                 3.01e-16
201.00
47.65%
32.94%
18.51%
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (3778)..(4434)
                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1515)..(2081)
                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (2084)..(3745)
                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (4440)..(4712)
US-09-068-655-3
                                                                                                                                                                                    ORGANISM: Myxoma virus
                                                                                                                                                                                                                               LOCATION: (1)..(549)
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Best Local Similarity:
Query Match:
DB:
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FEATURE:
                                                                                                                                                                       TYPE: DNA
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168 TCGTACGAATCCTACATCCGAAATATACGTACGATGCGGCGTTGCGTATACAGACAACGT 709
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                                                                                  Sequence 10, Application US/09068655A
Patent No. 6136579
GENERAL INFORMATION:
TEREATION:
APPLICANT: JACKSON, Ronald James
TITLE OF INVENTION: METHOD OF PRODUCING ALPHA 2,3-SIALYLTRANSFERASE
FILE REFERENCE: 026579-186
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: AU PN 6587
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1995-11-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PAPENTICATION NUMBER: PCT/AU96/00725
SATURER PEDICATION NUMBER: PCT/AU96/00725
SATURER PEDICATION NUMBER: PCT/AU96/00725
SEQ ID NO 10
EENGTH: 1806
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Matches:
Conservative:
Mismatches:
Indels:
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                  572 ------TACGTACTGGAACTCTAC 589
175 GlnLeuArgArgIleLeuLeuProLeuTyr 184
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Sequence 3, Application US/09068655A
Patent No. 6136579
GENERAL INFORMATION:
APPLICANT: JACKSON, Ronald James
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87.50
41.07%
33.93%
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; LOCATION: (1405)..(1806)
US-09-068-655-10
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Myxoma virus
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (2)..(439)
FEATURE:
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Best Local Similarity:
                                                                     09-068-655-10/c
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998 TGGTTCCGTTCAAGTCCGCCGACTTATACTGGCTATATAACATGCTTACGAACAACAACGCAC 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ACGTGTGCCAGG-----GCGTAACGATTACGGGATTCGGGTACCCCAATGGGGGGCCTA 711
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TITLE OF INVENTION: METHOD OF PRODUCING ALPHA 2,3-SIALYLTRANSFERASE CURRENCE: 026579-186
CURRENT APPLICATION NUMBER: US/09/068,655A
CURRENT FILING DATE: 1996-08-31
EARLIER FILING DATE: 1996-08-31
EARLIER FILING DATE: 1995-11-15
EARLIER FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PARLIER PLILING DATE: 1200-11-15
NUMBER OF SEQ ID NOS: 13
LENGTH: 4713
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AspCysAlaArgHisValAlaAspPheLeuArg-----GlyAsnPro-
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Conservative:
Mismatches:
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100 GlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeuTyrPheCysGluAspArg 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 TrpPheThrSerTrpSerProCysTyrAspCysAlaArgHisValAlaAspPheLeuArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 ------GCCTGGTACCGCATCGCGGACGGGTGCGCACCTCCTGTTTTTCGAG
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                                                                                                                                           r.
                                                                                                                                          APPLICANT: PETROVSKIS, ERIK A.: POST, LEONARD E.:TIMMINS, JAMES TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN NUMBER OF SEQUENCES: 12
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42
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/513,282
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: 1100,817
FILING DATE: 29-JUN-1987
APPLICATION NUMBER: 886,260
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 784,787
FILING DATE: 16-JUL-1986
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 801,799
FILING DATE: 26-NOV-1985
APPLICATION NUMBER: 844,113
FILING DATE: 26-NOV-1986
FILING DATE: 26-NOV-1986
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4041 TTTTGTCGT 4049
                 63
                 61 PheLeuArg
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Best Local Similarity:
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5352575-4
;Patent No. 5352575
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FLING DATE: 23-DEC-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
               ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFRENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 123:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7077 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5
80.00
47.62%
34.92%
7.37%
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LOCATION: 1...7077
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                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN
                                                                                     COUNTRY: USA
ZIP: 94304-1018
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-221-017B-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
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REAGENTS AND METHODS FOR THE USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
                                                                                            114 TyrPheCysGluAspArgLysAlaGluProGluGlyLeuArgArgLeuHisArgAlaGly 133
              94 ValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeu 113
                                                  271 TICCTICCAATICTCAGG-----AATIAATATAGATACATITITGAAAAAAAATCT 221
                                                                                                                                                                       134 ValGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGlu 153
                                                                                                                                                                                                               184 AGTCACCATATCCTCTATTTGTTCAATTATTTTTCATCTTCGGCACACTAGGATCTAT 125
                                                                                                                       154 AsnHisGluArgThrPheLysAla---TrpGluGlyLeuHisGluAsnSerValArgLeu
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049.69R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: BILLING-MEDEL, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6068.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Abbott Laboratories: 100 Abbott Park Road Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/09049698 Patent No. 6368792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/828,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 601
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAYDEN, MARK
APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SEAGENT
TITLE OF INVENTION: USEFUL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                  173 SerArgGln 175
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64 GTGCAGCAG 56
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US-09-049-698-18/c
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APPLICANT:
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US-09-049-698-18
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APPLICANT: HAYDEN, MARK
APPLICANT: HAYDEN, MARK
APPLICANT: HAYDEN, MARK
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 TGCAACTATAACATCAGCATGTTTAGGTTTTTCATGTTTTTGGCCTTTTTGTACTGAGGATT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TGTAGGTGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 -----TyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-966-880A-8 (1-198) x US-09-049-698-16 (1-3043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEO TO Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,698
  652 ATGCGATTCCTGACGCCGTTCTACCAG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,856
FILING DATE: 31-MAR-1997
ATTONNEY,AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
FEBERBENES/DOCKT NUMBER: 6068.US.P1
TELECOMUNICATION INFORMATION:
                                                                                                                                        APPLICANT: BILLING-MEDEL, PATRICIA A. APPLICANT: COHEN, MAURICE APPLICANT: COLPITTS, TRACEY L. APPLICANT: FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                 Sequence 16, Application US/09049698
Patent No. 6368792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3043 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.50
43.09%
26.02%
6.95%
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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                                                          US-09-049-698-16/c
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STATE:
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                                                                                                                                                                                                                                                                                                                       282 TTCCTTCCAATTCTCAGG-----AATTAATATAGATACATTTTGAAAAAAATCT 232
                                                                                                                                                                                                                                                                                                                                                                                  134 ValGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheValGlu 153
                                                                                                                                                                                                                                                                                                                                                                                                          195 AGTCACCATATCCTCTATTTGTTCAATTATTTTTTCATCTTCTGGCACACTAGGATCTAT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AsnHisGluArgThrPheLysAla -- - TrpGluGlyLeuHisGluAsnSerValArgLeu 172
                                                                                                                                                                                                                                   342 TGCAACTATAACATCAGCATGTTTATGGTTTTCATGTTTTGGCCTTTTGTACTGAGGATT 283
                                                                                                                                                                                                                                                                 94 ValAlaAspPheLeuArgGlyAsnProAsnLeuSerLeuArgIlePheThrAlaArgLeu 113
                                                                                                                                                                                                       76 -----TyrArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArgHis 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARLEL NO. 30.303.

GENERAL INFORMATION:

APPLICANT: B vik, Claes Olof, Eriksson, Ulf

TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which

TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding

TITLE OF INVENTION: Therefor, And Uses Thereof

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue
               3181
32
21
49
21
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                 US-09-966-880A-8 (1-198) x US-09-049-698-18 (1-3181)
                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/883,539
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, no. 5573939man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 280
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08200807
Patent No. 5573939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS
             19.8
75.50
43.09%
26.02%
6.95%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 SerArgGln 175
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COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GTGCAGCAG 67
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                                          Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 ValGluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824 ------TGGGGAGCCAATTACATGGATTGTTTTGAATCCAATGAAACCATGGGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        902 ---AAAAAGTATATCAATAATAAATACAGGACCTCTCTTTTAACCTC-----TTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 -----CysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         995 CICTGTTGCTGGAAAGGATTTGAATTTGTTTATAATTATTATATTAGCCCAATTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 -----TrpGluGlyLeuHisGluAsnSerValArgLeuSerArg----GlnLeuArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 ArgValThrTrpPheThrSerTrpSerProCysTyrAspCysAlaArg------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: B vik, Claes Olof; Eriksson, Ulf; Peterson, Per A.
TITLE OF INVENTION: Isolated Protein Receptors, Antibodies Which
TITLE OF INVENTION: bind Thereto, Nucleic Acid Sequence Coding
Patent No. 56/9772
TITLE OF INVENTION: Therefor, And Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STRET: New York City
STRET: New York City
STRET: New York
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875 TGGCTTCATATTGCTGACAAAAAAGA------
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
(212) 688-9200
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                  TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 bases
                                                                                                                                                                                                                                                                                                                 26.8
73.50
37.938
20.008
6.778
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                          ; ANTI-SENSE: no
US-08-200-807-1
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-488-305A-1
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995 CTCTGTTGCTGGAAAGGATTTGAATTTGTTTATATTATTATTATTAGCCAATTTACGT 1054
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                       MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage COMPUTER: IBM PS/2
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Matches:
Conservative:
Mismatches:
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                                    COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,305A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KOAll, VINEET
REGISTRATION NUMBER: JUD 5280.3
REFERENCE/DOCKET NUMBER: JUD 5280.3
REFERENCE/DOCKET NUMBER: JUD 5280.3
REFERENCE/DOCKET NUMBER: JUD 5280.3
REFERENCE/OCKET NUMBER: JUD 5280.3
REFERE
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20.00%
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
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HYPOTHETICAL:
ANTI-SENSE:
US-08-488-305A-1
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Search completed: June 19, 2003, 19:04:05 Job time : 59 secs

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Run on:

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Sequence 113, App Sequence 699, App Sequence 268, App Sequence 128, App Sequence 1372, A Sequence 5061, Ap Sequence 5061, Ap Sequence 4504, Ap Sequence 4504, Ap Sequence 5737, Ap Sequence 5737, Ap Sequence 5737, Ap Sequence 6443, Ap Sequence 6443, Ap Sequence 1443, Ap Sequence 15, Appl Sequence 25835, Ap Sequence 25835, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 221, App
Sequence 9282, Ap
Sequence 5098, Ap
Sequence 19, Appl
Sequence 15, Appl
           US-09-864-761-9282
US-09-783-590-5098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09966880A

Patent No. US20020164743A1

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVEWTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24

PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FILING DATE: 1999-06-24

PRIOR FILING DATE: 1999-06-24

PRIOR FILING DATE: 1999-03-29

NUMBER: OF SEQ ID NOS: 36

SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-166-087-49
US-10-080-960-15
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NAME/KEY: CDS
LOCATION: (80)...(673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-966-880A-7
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LENGTH: 28:
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-MODEL-frame+_pAn.model.-DEV-xlh
-Q-Agn2_1/USPTQ_spool/US09966880/runat_14062003_175646_16343/app_guery.fasta_1.391
-Q-Agn2_1/USPTQ_spool/US09966880/runat_14062003_175646_16343/app_guery.fasta_1.391
-QO-Agn2_1/USPTQ_spool/US09966880/runat_14062003_175646_16343/app_guery.fasta_1.391
-DB-Published_Applications_NA -OFMT-fastap -SUFFIX-P2n.rnpb -MINMATCH=0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -STRAT=1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -TR-SCORE-pct -THR_MAX.EN-0
-MAXLEN-200000000 -USR-EN-S09966880_GCGN_11_57_erunat_14062003_175646_16343
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5
-FGAPOP-6 -FGAPEXT=7 -YGAPOP-10 -YGAPEXT=0.5 -DELOP-6 -DELEXT=7
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Sequence 1, Appli
Sequence 10, Appl
Sequence 35, Appl
                                                                                                                           (without alignments)
1862.504 Million cell updates/sec
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                                                                                                                                                                                     1086
1 MDSLLMNRRKFLYQFKNVRW.....ILLPLYEVDDLRDAFRTLGL 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           June 19, 2003, 17:54:11; Search time 156 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                           nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-966-880A-7
US-09-966-880A-1
US-09-966-880A-10
US-09-966-880A-35
                                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
                                                                                                                                                                       US-09-966-880A-8
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Searched:

4.0

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PRIOR APPLICATION NUMBER: JP 11-178999
PRIOR FLING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: JP 11-87192
PRIOR FILING DATE: 1999-03-29
                                  NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version
                                                                           ORGANISM: Mus musculus
                                                  SEQ ID NO 1
LENGTH: 2440
                                                                    TYPE: DNA
                                                                                   FEATURE:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hondo, Tasuku
APPLICANT: Hondo, Tasuku
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR APPLICATION NUMBER: JP 11-371382
PRIOR APPLICATION NUMBER: JP 11-371382
                                                                           Length:
Matches:
                                                                                                                    Gaps:
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                                                                           6.66e-142
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                                ; NAME/KEY: 3'UTR
; LOCATION: (677)...(2818)
US-09-966-880A-7
        NAME/KEY: 5'UTR
LOCATION: (1)...(79)
                                                                                           Percent Similarity:
Best Local Similarity:
                                                                    Alignment Scores:
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1542 IGGGAGAATATTATCAGCTIGTCCAAGCAAAATTTTAAATGTGAAAAAAAAAA	52 52	1602 TTAAGCATTTTTGAAAATTAAGGAAGAAGAATTTGGGAAAAATTAACGGTGGTTCAATT 1661	52 52	1662 CIGITITCCAAATGATTICTTTTCCCTCCTACTCACATGGGTCGTAGGCCAGTGAATACA 1721	52 52	1722 TTCAACATGGTGATCCCCAGAAAACTCAGAGAAGCCTCGGCTGATGATTAATTA	52 52	1782 TCTTTCGGCTACCCGAGAGATTACATTTCCAAGAGACTTCTTCACCAAAATCCAGATGG 1841	52 52	1842 GTTTACATAAACTTCTGCCCATGGGTATCTCCTCTCTCTAACACGCTGTGACGTCTGGG 1901	52 52	1902 CTTGGTGGAATCTCAGGGAAGCATCCGTGGGGTGGAAGGTCATCGTCTGGCTCGTTGTTT 1961	52 52	1962 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 2021	52 52	2022 CCTTCCTATTCGGTGACATGACACATTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 2081	52 52	2082 ITCATTTACTTCTCATGGCAGTGCCTATTACTTCTCTTACAATACCCATCTGTCTG	52 52	2142 ACCAAAATCTATTTCCCCTTTTCAGATCCTCCCAAATGGTCCTCATAAACTGTCCTGCCT 2201	52 52	2202 CCACCTAGTGGTCCAGGTATATTTCCACAATGTTACATCAACAGGCACTTCTAGCCATTT 2261	52 52	2262 TCCTTCTCAAAAAGGTGCAAAAAAGCAACTTCATAAAACACAAATTAAATCTTCGGTGAGGTA 2321	52 52	2322 GIGIGAIGCIGCTICCTCCCAACTCAGCGCACTICGTCTTCCTCATTCCACAAAAACCCA 2381	52 52	2382 TAGCCTTCCTTCACTCTGCAGGACTAGTGCTGCCAAGGGTTCAGCTCTACCTAC	52 52	2442 GCTCTTTTGAGCAAGTTGCTTAGCCTCTCTGTAACACAAGGACAATAGCTGCAAGCATCC 2501	52 52	2502 CCAAAGATCATTGCAGGAGACAATGACTAAGGCTACCAGAGCCGCAATAAAAGTCAGTGA 2561	53	2562 ATTTTAGCGTGGTCCTCTCTGTCTCTCCAGACGGCTGCCACGTGGATTGCTCTTCCTC 2621	63 ArgTyrIleSerAspTrpAspLeuAspProGlyArgCysTyrArgValThrTrpPheThr 82
qa	Qy	qq	Qy	QQ	Qy	QQ	QY	qa	δλ	qq	Qy	qa	Qy	QO	Qy	qq	Qy	qq	Οy	qa	δý	qq	οy	qa	Qy	qa	Qy	QQ	οy	QQ	Qy	qa	Qy	QQ	Qy Dp
Db 633 TIGCCCTFGTACGAAGTCGATGACTTGCGAGATGCATTTCGTATGTTGGGA 683	RESULT 3	US-09-966-880A-10 Sequence 10, Application US/09966880A	; Facelc NO. 052020104/45A1; Shriet NO. 052020104/45A1; Shriet Sh	APPLICANT: HORJO, Tasuku ; APPLICANT: HUramatcu, Masamichi ; Tapip Op Tarbumatou, Noter competing Charters	; IIILE OF INVENTION: NOVEL CITIDINE DEAMINASE ; FILE REFERENCE: 06501-088001.	; CURRENI AFFLICATION NUMBER: US/US/900,88UA ; CURRENT FILING DATE: 2001-09-28	; PRIOR FILING DATE: DATE: 11.271200. 0.12120	; FRION REFLICATION NUMBER: JF 11-3/1302 ; PRIONE FILING DATE: 1999-12-27 ; DETAC ADDITAMENTAL HTMLDED: 11-1-120000	-87162	; PRIOR FILING DATE: 1999-03-29	FastSEQ for		CREATISM: Homo sapiens	Alignment groves.		octor Similarity: 24.02% Conservative:	59.35%	.09-966-880a-8 (1-198) x IIS-09-966-880a-10 (1-6564)	To Laboration I was a few many and the second	106		1123 GGTCGGCGTGAGACCTGTGCTACGTAGTGAAGAGGCGTGACAGCGTACATCCTTT			57	こと 1242 THTAATGGTCAACTGTGAGTGCTTTTTAGAGCCCACCTGGTGGTATTTAGAGCCTACTTTTTAGAGCCCACCTTGTTAATTTAGAGCCCACCTTGTTAATTTAGAGCCCACCTTGATTGA	25	70 000000000000000000000000000000000000	1502 TTTTGGCATTTGTGTCTCTACACATTCTCTTTTTTTTTT	52	100 ICCALCCARALITAGACALGGGCCCARARALATGGGATITARATICCICCCCAGGTAATGC	76		1482 CCAGCTTTCCTCAGCATCTGAATTGCCTTTGAGATTAATTA	52 52

Query Match: 59.35% Indels: 560 DB: 9 Gaps: 2 US-09-966-880A-8 (1-198) x US-09-966-880A-35 (1-11204)	LeuLeuMetAsnArgArgLysPheLeuT 	Oy 23 GlyArgArgGluThrTyrLeuCysTyrValValLysArgArgAspSerAlaThrSerPhe 42	Qy 43 SerLeuaspPheGlyTyrLeuargasnLys 52		Db 6457 TTTAATGGTCAACTGTGAGTGCTTTTAGAGCCACCTGGTGTATTACTTCCATCCTT 6516	ζγ 52 52	Db 6517 TTTTGGCATTGTGTCTCTATCACATTCCTCAAATCCTTTTTTTT	ογ 52 52	Db 6577 TCCATGCACCCATATTAGACATGGCCCAAAATATGTGATTTAATTCCTCCCCAGTAATGC 6636	ογ 52 52	Db 6637 TGGGCACCCTAATACCACTCCTTCAGTGCCAAGAACAACTGCTCCCAAACTGTTTA 6696	Qy 52 52	Db 6697 CCAGCTTTCCTCAGCATTGCCTTTGAGATTAATTAAGCTAAAAGCATTTTATA 6756	Ογ 52 52	Db 6757 IGGGAGAATATTATCAGCTTGTCCAAGCAAAAATTTTAAATGTGAAAAACAAATTGTGTC 6816	φγ 52 52	Db 6817 TTAAGCAFTTTTGAAAATTAAGGAAGAATTTGGGAAAAAATTAACGGTGGTTCAATT 6876	Ολ 52 52	Db 6877 CTGTTTTCCAAATGATTTCTTTTCCCTCCTACATGGGTCGTAGGCCAGTGAATACA 6936	Δy 52 52	Db 6937 ITCAACATGGTGATCCCCAGAAAACTCAGAGAAGCCTCGGCTGATGATTAAATTAAATTGA 6996	Qy 52 52	Db 6997 TCTTTCGGCTACCCGAGAGAATTACATTTCCAAGAGACTTCTTCACCAAAATCCAGATGG 7056	Qy 52 52	Db 7057 GTTTACATAAACTTCTGCCCATGGGTATCTCCTCTCTCTAACACGCTGTGACGTCTGGG 7116	Qy 52 52	Db 7117 CTTGGTGGAATCTCAGGGAAGCATCCGTGGGGTGGAAGGTCATCGTCTGGCTCGTTGTTT 7176	Oy 52 52	Db 7177 GATGGTTATATTACCATGCAATTTTCTTTGCCTACATTTGTATTGAATACATCCCAATCT 7236	Оу 52 52	Db 7237 CCTTCCTATTCGGTGACATGACACATTCTATTTCAGAAGGCTTTGATTTTATCAAGCACT 7296
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4 × 4 81.0 H	## APPLICANT: Muramatsu, Masamichi ## TITLE COF INVENTION: NOVEL CYTIDINE DEAMINASE ## FILE REFERENCE: 06501-08801 ## CURRENT APPLICATION NUMBER: US/09/966,880A ## CURRENT PILICA DATE: 2001-09-28 ## PRIOR APPLICATION NUMBER: DCT/TP00/01918 ## PRIOR APPLICATION NUMBER: UP 11-371382 ## PRIOR FILING DATE: 1999-03-28 ## PRIOR FILING DATE: 1999-03-29 ## PRIOR PRIOR PAPELICATION NUMBER: DEBTE DATE:	US-09-966-880A-8 (1-198) x US-09-966-880A-13 (1-271) Qy 53 AsnGlyCysHisValGluLeuLeuPheLeuArgTyrIleSerAspTrpAspLeuAspPro 72 1	SULT 6 -09-729-674-173 Sequence 173, Application US/09729674 Patent No. US20010039335A1 APPLICANT: Jacobs, Kenneth APPLICANT: Jacobs, Kenneth APPLICANT: LaVallie, Edward R. APPLICANT: Collins-Racie, Lisa A.
52	7477 TCCTTCTCAAAAGGTGCAAAAAGCAACTTCATAAACACAAATTAAATCTTCGGTGAGGTA 7536 52	7897 TCCTGGAGCCCCTGCTACGACTGTCCCCACTTTTTTGCGGGGAACCCC 7956 103 AsnLeuSerLeuarg11ePherthralaargLeuTyrPhecysGluspargLuspalaGlu 122	CCTCTGGAGCCGAAATTAAAGATTAGAAGCAGAGAAAAGGGTGAATGGCTCAGAGACAAG GCCCCGAGGAAATGAGAAAATGGGGCCAGGGTTGCTTTTCCCCTCGATTTGGAACCTG AACTGTCTTCTACCCCCCATATCCCCGCCTTTTTTTTTT

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RESULT 8
US-10-098-841-268
; Sequence 268, Application US/10098841
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Best Local Similarity:
Query Match:
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                             -09-925-300-699
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APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Steininger II, Robert J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64x
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
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US-09-729-674-173
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                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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Mismatches:
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Sequence 699, Application US/09925300 Patent No. US20020151681A1
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369.50
58.52%
44.89%
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                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Homo sapiens US-09-925-300-699
                                                                                       Steve Ruben
                                                               APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
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| TIGATGGATCCACACATATCACTTCCAACTTTAACAAT------GGCATTGGAAGG 159
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                  125 GlyLeuArgArgLeuHisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyr 144
                                                                                  145 PheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGly 164
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APPLICANT: HOTNE, Darci T
APPLICANT: HOTNE, Darci T
APPLICANT: OCKLEY, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 4921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 3282
LENGTH: 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Genbank Accession No. US20020142981A1 U03891
                                                                                                                                                165 LeuHisGluAsnSerValArgLeuSerArgGlnLeuArgArgIleLeu 180
                                                                                                                                                                 45 Asp-----PheGlyTyrLeuArgAsn-----LysAsn-----
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; Sequence 3282, Application US/09880107
; Patent No. US20020142981A1
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; LOCATION: (1)..(1348)
; OTHER INFORMATION: n
US-09-880-107-3282
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236 TTCACCGTGGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTGGAAGACG-----GGCGTC 289
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                                                                                                                                                                                                                                                                              APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: Pt_FL_genes Version 1.0
SEQ ID NO 268
LENGTH: 1143
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369.50
58.52%
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34.02%
No. US20020197679A1
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                                                                                                                             Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
                           APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
                                                                                                                                                                                              Wang, Dunrui
Wang, Zhiwei
Wehrman, Tom
Zhang, Jie
                                                                                                Zhou, Ping
Ma, Yunqing
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Best Local Similarity:
Query Match:
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152 lGluAsnHisGluArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSerValArgLe 172
                                                                                                                                                                                               132 aGlyvalGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsnThrPheVa 152
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09966880A

Sequence 12, Application US/09966880A

Sequence 12, Application US/09966880A

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatau, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERENCE: 06501-088001
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: DCT/JP00/01918
PRIOR APPLICATION NUMBER: PCT/JP00/01918
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-7
PRIOR FILING DATE: 1999-16-24
PRIOR FILING DATE: 1999-16-24

PRIOR FILING DATE: 1999-06-24

PRIOR APPLICATION NUMBER: JP 11-178999

PRIOR FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 36

SOFURWARE: FastSEQ for Windows Version 4.0
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Matches:
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                                                           113 LeuTyrPheCysGluAspArgLysAlaGluPro------GluGlyLeuArgArgLeu 129
                                                                                                                       130 HisArgAlaGlyValGlnIleAlaIleMetThrPheLysAspTyrPheTyrCysTrpAsn 149
                                                                                                                                                                                    ThrPheValGluAsnHisGluArgThrPheLysAlaTrpGluGlyLeuHisGluAsnSer 169
                                                                                          504
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Bostic, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Graham, James N.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402.
CURRENT APPLICATION NUMBER: 60/195,604
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR APPLICATION NUMBER: 60/195,604
SEQ ID NOS: 631
SOFTWARE: PATEORITY Ver. 2.0
SEQ ID NO 359
LENGTH: 2151
                                                                               505 CGGGATGCTGGGGCCCAAGTCTCCATGACCTACGATGAATTTAAGCACTGCTGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1397 CCAGGGCAGGGGTTTTCTATGCACCAGGCTCCACATAAACACGGTTTCCTT-----
                   GAAGTGCGTGCGTTCCTTCAGGAGAACACACGTGAGAACTGCGCGCTTTCGCTGCTGCCGC
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                                                                                                                                                                                                                                              26 GluThrTyrLeuCysTyrValValLysArg----
                                                                                                                                                                                                                                                                                                                                         Sequence 359, Application US/09822830A Patent No. US20020142952A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genetics Institute, Inc
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308.50
58.20%
42.86%
28.41%
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; ORGANISM: Homo sapiens
US-09-822-830A-359
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
FRICR APPLICATION NUMBER: US/207-18
FRICR APPLICATION NUMBER: 2002-07-18
FRICR APPLICATION NUMBER: 2001-07-18
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                                                     APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CONA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER: OF SEQ ID NOS: 38054
SOFTWARE: FSEQ ID NOS: 38054
SOFTWARE: FSEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 30237
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Publication No. US20030099974A1
GENERAL INFORMATION:
              Sequence 30237, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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257.00
58.97%
47.01%
23.66%
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US-09-918-995-30237
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US-09-918-995-30237
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Sequence 13, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION;
APPLICANT: Baranova, A. V.
APPLICANT: Kozlov, A. P.
APPLICANT: Kozlov, A. P.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequence.
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Conservative:
Mismatches:
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; LOCATION: 1, 2, 3, 1379, 1402, 1403, 1404
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13472
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13472
LENCTH: 1404
TYPE: DNA
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861 GGGAGATTCTC 872
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Best Local Similarity:
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119 CGTAAAGAGGCCTGTCTGCTCTACGAAATCAAGTGGGGCATGAGCCGGAAGATCTGGCGA 178
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Fatent No. US20020164743A1
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Muramatsu, Masamichi
TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
FILE REFERRANCE: 06501-088001
CURRENT APPLICATION NUMBER: US/09/966,880A
CURRENT APPLICATION NUMBER: US/09/966,880A
FRIOR FILING DATE: 2001-09-28
FRIOR APPLICATION NUMBER: JP 11-371382
FRIOR FILING DATE: 1999-10-27
FRIOR FILING DATE: 1999-10-27
FRIOR FILING DATE: 1999-06-24
FRIOR FILING DATE: 1999-06-24
FRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 879
TYPE: DNA
ORGANISM: HOMO sapiens
US-10-157-031-13
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144 TyrPheTyrCysTrpAsnThrPheValGluAsnHisGluArgThrPheLysAlaTrpGlu 163
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Mismatches:
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Matches:
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ORGANISM: Homo sapiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_ov:*
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                                                                                                                                                                                                                                                                                                       GenEmbl:*
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
Sequence:
                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                 Searched:
                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

em_htgo_hum:* em_htgo_mus:*

em_htg_mus:* em_htg_pln:* em_htg_rod:*

em_htg_mam:* em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

NO.		Vuer y					
	Score	Match	Length	DB	DI	Description	lon
	54	99.4		σ	C09218	09218	Ø
7	4922.8	89.3	11204	σ (AB040430	AB040430	- 1
n =	ב ל		7 -	סת	AL160291	ALIOUZ91	= 0
* 10	5.5		1 -	, (AP002508	AP002508	: "
	41		7	σ	AC083783	AC083783	Homo sapi
c 7	41		5	6	AC005291	AC005291	Ω
	41	•	(*)	σ	AC104520	AC104520	Homo sap
	41	•	4	σ	AC053467	AC053467	Homo sap
Н.	41	•	17	~	AL590609	ALS90609	Homo sap
11	4.	٠	7	~	AL590728	AL590728	Homo sar
77	₹.	٠		7	ACU25620	ACU25620	HOMO Sap
13	\$	•	7	~	AC023132	AC023132	Homo sag
14	4	•	~	~	AC113194	AC113194	Homo sar
15	39	•	-	σ	AC069335	AC069335	Homo sar
-	39	٠	2	~	AC023786	AC023786	Homo sar
c 17	239	•	ω.	σ,	HS130N4	Z75887 HL	uman DNA
18	239	•	-	σ	AL390241	AL390241	Human DN
c 19	239	•	7	7	AC053473	AC053473	Homo sap
71	239	•	Ξ.	~	AC023411		Homo sap
~	239	•	Ξ:	6	AL354861	AL354861	Human DNA
c 22	~	•	~	7	AL391060	_	Homo sap
C	38	•		σ,	AL353665	_	Human DN
24	238.6	•	-	σ.	AC019129	_	Ношо зар
c 25	38	•		7	AL138818		Homo sap
26	36	•	4	0	AC090229	_	Homo sap
~	36	٠	7	o 1	AC007383		Homo sap
c 28	236	•	Ä	~	AC068746	_	Homo sap
~ (236	•	~ i	~	AC107202		Homo sar
יות	~!	•	7	7	AC107016		HOMO Sap
3.L	235.8	•	∹ ;	ט עב	ACU/43/5	_	HOMO Sap
3 6	ח ל	•	Η`	7 (AL512364		HOMO Sap
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4.0	4.	•	₹`	7	ACU32043		HOMO Sar
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39	33		H		0566	_	Homo sag
c 40	233.4	•	~		9978		HOMO Sag
41	33	•	w		99H1	_	Human DN
42	N	•	ä		6960		Homo sapi
43	32	•	H		Oldx	AL139021	Human c
44	232.4	•	ĭ		2	AC011271	Homo sap
c 45	32	•	H		C01054	AC010545	a

RESULT 1
AC092184
AC013443
ACCESSION
AC092184
AC013443
AC092184.7 GI:21206067
KEYWORDS
HTG.
SOURCE
Numan.
ORGANISM
HOMO sapiens
ELAFETER Prinates; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
AUTHORS
AUTHORS
ALSONOM, Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsonows, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Budaria, J., Bowde, S., Briewa, M., Brown, E., Brown, M., Bryant, N.P., Buday, C., Burch, F., Burkett, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Charez, D., Chavez, D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Edhaj, C., Enclistopoulos, C., Dedaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K., Delgar, D., Edwards, C.C., Elhaj, C., Parenting, S., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, F., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, P., Escotto, M., Falls, T., Ferraquto, D., Flagg, N., Ford, J., Foster, F., Escotto, M., Haris, C., Harris, C., Hall, M., Loilins, B., Homs, I.F., Howard, S., Huber, J., Hulyk, S., Hume, J., Dollivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, C., Levis, L.C., Levis, L.C., Levis, L.C., Levis, D., Lieu, G., Lieu, G., Lieu, G., Miller, A., Miner, G., Marchinez, E., Massey, E., Marchinez, E., McLeod, M., Lousey, M., Morris, S., Moser, M., Mohabbat, K., Mortgomery, K.T., Mortgomery, M., Morris, S., Moser, M., Mohabbat, K., Mortgomery, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M., P., Maccond, J., Newtson, J., Relfrod, B., Thomas, L., Peters, L., Pitkerson, E., Norde, M., Mortins, E., Wolde, R., Peters, L., Pitkerson, E., Norde, M., Mortins, S., Worter, J., Peters, L., Peters, J., Peters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 25, 2002 this sequence version replaced gi:20901754.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 71132)
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Direct Submission

Submissed (25-JUN-2001) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 71132)
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Direct Submission
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AUTHORS
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the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) seard of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (GNUC. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

standards - estimated error rate less than 1 per 10,000 bases. Reports of Lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality

```
complement(1. .1448)
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                                                                                                                                       function="clone overlap
                                           /organism="Homo sapiens"
                                                                                                                                                                                  439. 560
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774. 881
/rpt_family="MIR"
903. 1190
/rpt_family="AluSq"
1191. 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alusg"
4360. .4654
/rpt_family="Aluy"
complement(5140. .5262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5564. .5599
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5644. .5733
/rpt_family="MSTD"
                                                                                                                                                                                                                                                                                                                                                       /standard_name="8198"
1966. .2264
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3296. .3328
/rpt_family="(TTTC)n"
4097. .4249
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1591. .1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="FLAM_C" 5275, .5304
              Location/Qualifiers
                                                                                         /clone="RP11-438L7"
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                                                                            /chromosome="12
                                                                                                                                                                                                                                                                                                                                           1744. .1819
QUALSTAT-REPORT
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
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                                                                                                            misc_feature
                                source
              FEATURES
                                                                                                                                                        STS
                                                                                                                                                                                     STS
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of

gc-help@bcm.tmc.edu

Qy	1501 7	NGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA 1560			Ξ
qa	35459 T	TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA 35518	qq	36539 GACGAGAA	GAA
Qy	1561 CT	TITCCTAGGGAGGCGTTACTGAAATTATAGCTATAGTAAGAAAATTTGTAATTTTAG 1620	Qy	2641 AAGTTAAC	AAC
qa	35519 CI	CTITCCTAGGGAGGCGTIACTGAAATAATITAGCTATAGTAAGAAATITGTAATITITAG 35578	DÞ	36599 AAGTTA	AAC
Qy	1621 A	NATGCCAAGCATTCTAAATTAATTGCTTGAAAGTCACTATGATTGTGTCCATTATAAGG 1680	QY	2701 GAAACAGT	AGT(
qa	35579 AZ	AAATGCCAAGCATTCTAAATTAATTGCTTGAAAGTCACTATGATTGTGTCCATTATAAGG 35638	qa	36659 GAAACAGT	AGT
Qy	1681 AG	ACCAPATICATICAAGCAAGTIATITAATGTIAAAGGCCCAATTGTIAGGCAGTIAATG 1740	ΟŊ	2761 CCTTTATC	ATC
DÞ	35639 AG	AGACAAATTCATTCAAGCAAGTTATTTAATGTTAAAGCCCCAATTGTTAGGCAGTTAATG 35698	qa	36719 CCTTTA	ATC
Qy	1741 GC	ACTITIACIATIAACTAATCTTTCCATTTGTTCAGACGTAGCTTAACTTACCTCTAG 1800	δλ	2821 TAAGGCTC7	CIC
QQ	35699 GC	GCACTTTTACTATTAACTAATCTTTCCATTTGTTCACACGTAGCTTAACTTACCTTAG 35758	qa	36779 TAAGGC	CTC
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qa	35759 GT	GTGTGAATTTGGTTAAGGTCCTCATAATGTCTTTATGTGCAGTTTTTGATAGGTTATTGT 35818	QQ	36839 CACAAACA	ACAC
δ	1861 CA	TAGAACTTATTCTATTCCTACATTATGATTACTATGGATGTATGAGAATAACACCTA 1920	٥y	2941 CTCATCTAC	CTAC
qq	35819 CA	CATAGAACTIATICIATICCTACATITATGATTACTATGGGATGTATGAGAATAACACTA 35878	qq		CIPAC
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qa	35999 AA	GTCCTGGCCCAAGCGATCCTCCTGCCTGGGCCCTCCTAAAGTGCTGGAATTATAGACAT 36058	QQ O		rggr
Qy	2101 GA	GAGCCATCACATGCAATATACAGAATATATTTAATGGAGGATTTAATGTTCTTCAG 2160	ολ	3181 CTAATTATT 	FATT
q	36059 GA	GCCATCACATCCAGAATAACAGATTTTAATGGAGGATTTAATGGAGGATTTAATGTATGTTCAG 36118	q 0		LAT
ογ	2161 AA	AATTTCTTGAGGTCAGAATGTCAAATGTCTCCTCAGTTTACACTGAGATTTTGAA 2220	δλ	3241 AAAAGACAA	CAA
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Qy	2221 AA	CAAGTCTGAGCTATAGGTCCTTGTGAAGGGTCCATTGGAAATACTTGTTCAAAGTAAA 2280	Qy		TGA
QΩ	36179 AA	AACAAGTCTGAGCTATAGGTCCTTGTGAAGGGTCCATTGGAAATACTTGTTCAAAGTAAA 36238	qq	37259 CAGICTIGA	TGA
ογ	2281 AT	SGAAAGCAAAGGTAAAATCAGCAGTTGAAATTCAGAGAAAGACAGAAAAGGAGAAAAG 2340	ΟŊ	3361 ACAGTCATG	ATG
qq	36239 AT	ATGGAAAGCAAAAGTTAGCAGTTGAAATTCAGAGAAAGAGAAAAGGAGAAAAG 36298	qq	37319 ACAGTCATG	ATG
δy	2341 AT	SARATICAACAGGACAGAAGGGAAATATATATCATTAAGGAGGACAGTATCTGTAGA 2400	Qy	3421 TTTTAAAAT	AAT
qq	36299 AT	ATGAAATTCAACAGGAAGGAAATATATTATCATTAAGGAGGACAGTATCTGTAGA 36358	qa	37379 TTTTAAAAT	AAT
QY	2401 GC	CCATTAGTGATGGCAAAATGACTTGGTCAGGATTATTTTTAACCCGCTTGTTCTGGT 2460	Ολ	3481 TTTGCTGCC	- GCC
QQ	36359 GC	GCTCATTAGTGATGGCAAAATGACTTGGTCAGGATTATTTTAACCCGCTTGTTTCTGGT 36418	DÞ	37439 TITGCIG	000
οy	2461 TTC	SCACGGCTGGGGATGCTAGGGTTCTGCCTCAGGGAGCACAGCTGTCCAGAGCAGC 2520	Qy	3541 TAAAGTGAA	GAA
qa	36419 TTC	TTGCACGGTGGGGGATGCAGCTTGTGCTGCCTCAGGGAGCAGCTGTCCAGAGCAGC 36478	QQ .	499	GAA
οy	-	TGTCAGCCTGCAAGCCTGAAACACTCCCTCGGTAAAGTCCTTCCT	δ f	3601 GCTGAGGTG(GTG
Q		CAGCCTGCAAGCCTGAAACACTCCCTCGGTAAAGTCCTTCCT	2 3	ה ה ה	5 i
ογ	2581 GAC	GACGAGAACAGGGAGCTGGAAACAGGCCCCTAACCAGAGAAGGGAAGTAATGGATCAACA 2640	ŝ	3001 AACCCTGTT	- - -

CTAGCAGGTCAGGATCACGCAATTTCACTCTGACTGGTAACATGTGACA | GTAGGCTTATTGTATTTTCATGTAGAGTAGGACCCAAAAATCCACCCAAAGT ACACACCCGCCAACCAAGGTGCATGTAAAAAGATGTAGATTCTTGTGCTTT (TGGTTGGTACTATGGTAATTACCATAAAATTAWTATCCTTTTAAAATTAAAG **ICACAGCCCAGGAGGTAAGTTAATATAAGAGGGATTTATTGGTAAGAGATGA 1TTATGTGTGAGCTTATATACAAAGGGTTATTATATGCTAATATAGTAAT** GGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAA TATTGGATCTTTTTAGTATTCATTTTATGTTTTTATGTTTTTGATTTTTT **TAATATGGCTAATTTTTACCTTATGTAATGTGTATACTGGTAATAAATCTAG** CTAAAAGTTTAAAAGTGCTTTCCAATAAGCTTCATGTACGTGAGGGGAGACATT "TTCTATAACAAAAATTAGCCGGCCATGGTGGCATGTGCCTGTGGTCCCAGCT

OY 4801 CCACGCTGTACAGCTTGTGTTGCTGCAGCTGCAATGGGGACTCTTGATTTCTTTAA 4860	5041 CACACATGCAATCAGTATAATCCAAATCATGTAAATATGTGCCTGTAGAAGACTAGAGG 5 11111111111111111111111111111111111	09 5341 AYCATAGCTCACTGCACCTCTGTTGTTGCCCATGCTGCAGTGCAATGCCATG 39294	AB040430 LUCUS AB040430 LUCUS BOUNDED LUCUS AB040430 LUCUS ACCESSION AB040430 LUCUS ACCESSION AB040430.1 GI:9988407 KEYWORDS ADD: activation-induced cytidine deaminase. ACCESSION AB040430.1 AB04040.1 AB0
619 AACGCTGTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCCCAGCT 721 ACTAGGGGGCTGAGGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAG 679 ACTAGGGGCTGAGCCAGGAGTCAAGGAGCTGCAGCAGCAG 781 TGCTTGGGCTGCAGCCAGGAGCCCAGGAGGTCAAGAAAAAAA 781 TGCTTGGCGCTGCACCCGGCTGGCTGCACAGAGCAGACCAGACCTTGCCTCCAAAAAAAA	3/859 TTAGTTAGGCTGATATTTTGGTATTTTAAAGTCAGGGTCTGCACCTAC 37918 3961 ATTATTAAAATATCAATTCTCAATGTATACCTTTTAAAGTCGGGTCTGCACTAC 37918 3961 ATTATTAAAATATCTCAATGTATATCCACAAAGACTGGTACGTGAATGTTCAT 4020 11111111111111111111111111111111111	38155 AGGGATAATGTATGCCATACGAAATTCTAGAAAGTAACTTATTTTTTTT	441 GACTGCAAAGAGGAACAAGCTCTGGTGGGTGGTGATTCAGGTTCTGTATCCT 4500 38395 GACTGCAAAGAGGGAAGAAGCTCTGGTGGGTGGTGATTCAGGTTCTGTATCCT 38454 4501 GACTGTGGTAGCAGAAGCTCTGGTGGGTGGGTGGTGATTCAGTTCTTATCCTA 4560 11111111111111111111111111111111111
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and Durandy,A. TITLE Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2) Cell 102 (5), 565-575 (2000) MEDLINE 20460541 AUTHORS Muto.T. Muranatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T. AUTHORS Muto.T., Muranatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T. JOURNAL Submission JOURNAL Submitted (18 MAR-2000) Tasuku Honjo, Kyoto University, Department of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku, Kyoto, Kyoto 606-8501, Japan (E-mail:honjo@mfour.med.kyoto-u.ac.jp, Tel:81-75-753-4371/ex.4371), Fax:81-75-753-4388) Location/Qualifiers Source /organism-*Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /dp_aref="taxon:9606" /gene="AlD" /gene	3305 a 3305 a 3421; Conse 4921; Conse 591 AGGTTCAG	AATAACCCAAGAAGCTATTTAAATGCTCTTTAAGGTATTTACATAATATTACTATTCTC AATAACCCAAGAAGCTATTTAAATGCTCTTTAAGGTATTTACATAAATATTACTATTCTC ATGGCTTTTATTTGTGTTATCATGATTATAAGGTATTTACATAAATATTACTATTCTC ATGGCTTTTATTTGTGTTATCATGATTATAATGAAGTGTCTACTGTTACTGCTCC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2
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Direct Submission

AL Submitted (13-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Muring sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with responding to the overlapping clone, as we submit sequences with ris sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-

30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The folluwing abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wer, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGP/Chr10

RP11-85618 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
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Best Local Similarity 50.3
Matches 1030; Conservative
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CGGGTAGATGGGATTACAGGCGCCCACCACCACACTCGGCTAATGTT 5447 GGTGAATGATAAAAATACAAAAACCGAGAACATTTATTGAGTGT 109553 CCAAGATCTTGCTTTTGCATAATGATTCAGAGCAAATCAAATGGTT 109793 CAGGGGATAACAGTATACTGGATGTTGTCCAACAACAAGTACCATTTG 109913 ATGGAGAAACCACAGTTTAAAATGGTCACTTATTTAAATAACACAAA 109433 CATCAAAAGTCTAATCTCAAAATATCTTCAGTAAGTCAACCAAATAT 109493 5267 161776 bp DNA linear PRI 06-APR-2001 ence from clone RP5-1167E19 on chromosome 20 Contains a CpG island, complete sequence. AACTIGGGITACCAGAGIATITCCACAAATGCTATICAAATTAGIGC 4910 GACACTGTGCTAGGAGCCAGAAAACAAAGAGGAGGAGAAATCA--GT 4968 TITITITITITITGAGAIGGAGITITIGGICTIGIIGCCCAIGCIGGA 5327 CGCTGTACAGCTTGTGTTGCTGTCTGCAGCTGCAATGGGGACTCTTG 4850 AYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAAGCTGT 5387 GCATTICTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCT 4790 CAACATAGCAAGATATTTAGATCATTTTGACTAGTTAAAAAAGCAGC ACACATGCAATCAGTATAATCCAAATCATGTAAATAT-GTGCCTGTA AATAAACACAAAAATCTTAACAGTCATTGTCATTAGACACTAAGTCT ATTTTTCCATAGTATTCAAGTTTGACAATGATCAAGTATTACTCTTT 0

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        CEBLO 1554, UK. E-mails enquirites: numquery esanger.ac.uk clone requests: clonerequestesanger.ac.uk
On Jun 14, 2000 this sequence version replaced gi:8517286.
On Jun 14, 2000 this sequence version replaced gi:8517286.
On Jun 14, 2000 this sequence version replaced gi:8517286.
On Jun 14, 2000 this sequence version replaced gi:8517286.
On Jun 14, 2000 this sequence version motations
Where differences are found these are annotated as variations
together with a note of the overlapping clone, as we submit sequences such together with any not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their sequences with numbers given in the feature table with their sequence adaptases:

Em: EMBL; Swr.; SMISSPROT; Tri. TREMBL; Wp:, WORMPEP: Information numbers given in the feature table with their sequence
was generated from part of bacterial clone contigs of human chromosome 20. constructed by the Sanger Centre Chromosome 20. constructed by the Sanger Centre Chromosome 20. frits sequence is the entire insert of clone RP5-1167E19 The true left end of clone RP1-179J15 is at 93503 in this sequence.

This sequence is the entire insert of clone RP5-1167E19 The true clone RP1-179J15 at 193803 in this sequence.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were entered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by high quality data (i.e., phred quality) as sembly was confirmed by restriction digest. RP5-1167E19 is from first-hard resolated by the group of Pieter de Jong. For first-hard resolated by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .525 of consensus"
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/note="HAL1 repeat: matches 425. .559 of consensus"
3404. .3703
/note="AluSq repeat: matches 1. .300 of consensus"
comptement(3553. .4081)
/note="match: GSS: Em:B95838"
complement(3631. .4052)
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UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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note="AluSx repeat: matches 1. .290 of consensus"
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1807. 1893
//note="MIR repeat: matches 39. .122 of consensus"
2601. .2693
//note="HALI repeat: matches 5. .98 of consensus"
2743. .2880
//note="IRA45 repeat: matches 389. .525 of consens
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/note="28 copies 2 mer ag 76% conserved"
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'note="HAL1 repeat: matches 559.
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/note="match: GSS: Em:AQ729312"
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/note="match: STS: Em:Z67317"
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/db_xref="taxon:9606"
/chromosome="20"
/clone="RP5-1167E19"
/clone lib="RPCI-5"
145. 449
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/note="15 cop
1807. .1893
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/note="L2
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14119. 14269

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10912 .11493
/note="L2 repeat: matches 1396. .2019 of consensus"
11505 .12032
/note="L2 repeat: matches 2208. .2738 of consensus"
12058 .12368
/note="Alusq repeat: matches 1. .311 of consensus"
complement(12727. .13254)
/note="match: GSS: Em:AQ714903"
13528 .13670
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                                                                                                                                                                                                                      9884. 10018
/note="L2 repeat: matches 1262. 1398 of consensus"
10076. 10172
/note="MirlJ repeat: matches 104. .200 of consensus"
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/note="LTR33 repeat: matches 294. .521 of consensus"
10824. .10911
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                                                                           8631. .8827
/note="12 repeat: matches 739. .939 of consensus"
8828. .9148
/note="hlly repeat: matches 1. .309 of consensus"
9149. .9501
                                                                                                                                                                             /mote="Alujo repeat: matches 1. .297 of consensus"
complement(23846. .24267)
/hote="match: GSS: Em:AO562784"
complement(23854. .24167)
  consensus"
                                           .188 of consensus"
  ot
.169
repeat: matches 47.
                                      /note="MIR repeat: matches 27.8058. 8267
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Oy 3711 GGTCCCAGCTACT-AGGGGCTGAGGCAGGAATCTTTGGAGCCCAGGAGGTCAAGGCT 3769 Db 29558 AATCCCAGCTACTCAGGAGGCTGAGGACTCACTTGAACCCTGGAGGCCAAAGTT 29617 Oy 3770 GCACTGAGCATGCTGCGCCACTCCACCTGGAGGCCAAGGCT 3829 Db 29618 GTGGTGAGCTGCCCATGCACCTCCAGCCTGGGTGACAGACCTTGCT 3829 Db 29618 GTGGTGAGCTGGCCATGCACCTCCAGCCTGGGCAACAAGACTC 29677	QY 3830 CAAAAAAATAAGAAGAAAATTAAAAATAAATGGAAACAACTACAAAGAGCTGTTGTCCT 3889 LI	Oy 3950 ACCTGCACTACATTATAAAATATCAATTCTCAATGTATATCCACAAA-AGACTGGTAC 4008 DD 29798 TGATATCTGATATAAATGACACACAACATTGCAGGTAAGTGGAGAAAGATAGGCTTTT 29857 OY 4009 GTGAATGTTCATAGTACCTTTATTCACAAAACCCCCAAAGTAGAGACTATCCAAATATCCA 4068	4069 TCAACAAGTGAACAAATATGGCTATATCCATGCAATGGAATACCACCTGCA 1 1 1 1 1 1 1 1 1 1	4189 CAGACATGAAGGAGGATAATGTATGCCATACGAAATTCTAGAAAATGAACTTA	OY 4309 GAGAGGC-CACGTGGGAAGTTGCTAGAACTCAGGAGTTCAAGACCAGCCTGGGCAACAC 4367	4428 TGGGGAGGGAAGGACTGCAAAGAGGGGAAGAAGCTCTGGTGGGGTGAGGGTGATTCA	0.5 0.5
		5 602 238. 5727	repeat_region 2696127518 /note="HAL1 repeat: matches 4891090 of consensus" repeat_region 2797628337 /note="LIME3 repeat: matches 37944167 of consensus" repeat_region 2833828529 /note="MLTID repeat: matches 1192 of consensus" repeat_region 2867628918	28919 .29225 / Anote-"AluSx repeat: matches 1309 of consensus" 29226 .2939 / Anote-"LimE3 repeat: matches 45934759 of consensus" 29398 .29709 / Anote-"AluSp repeat: matches 1313 of consensus" 2971030118 / Anote-"LimE3 repeat: matches 47595157 of consensus"	repeat_region 3011930247 Query Match	Db 29141 GTCTCGAACTCCTGAGCTCAGGCAATCTGCCCACCTCAGCCTCCCAAAGTGCTAGGATTA 29200 QY 3362 CAGTCATGAGCCATGCATCTGGCCTAGGATCAGTTAAAATAGTTAAAAT 3421 Db 29201 CAGGTGTGAGCCACTGTGCCCAGCCGACTTTACTGCAGTTCTAATCAACATT 29260 QY 3422 TTTAAAATAATGGCTAATTTTACCTTATGTAATGTGTAATCAGGTAATAAACTAGT 3481 Db 29261 TCTTTGGAACTTAAGCTGATTTTTACCTTATGTAATGTGTAATAAAATAAAATGTGTAATAAAATAAAGAAAAGTAAAAGAAAAAG 29317	Qy 3482 TTGCTGCCTAAAGTTTTAAAGTGCTTTCCAATAAGCTTCATGTACGTGAGGGAACATTT 3541 Db 29318 ACACAGTGAAAAATGGGTGGACTCACCCTAGGATACAACAAGT 29377 Qy 3542 AAAGTGAAAAAGGCAAAATGGGTGGCTCACGCCTGTAATCCAGCACTCT 3595 I I I <

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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
            nitted (09-JUN-2000) Masahira Hattori, The Institute of Physical Chemical Research (RIKEN), Genomic Sciences Center (GSC); asato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: PCR products; 100% of reads chemistry: Dye-terminator Er-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 166893 bases at least Q40 Consensus quality: 174794 bases at least Q30 Consensus quality: 178794 bases at least Q30 Insert size: 181472; sum-of-contigs Quality coverage: 4.40x in Q20 bases; sum-of-contigs
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                                                                Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagaa
Japan (E-mall:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923
Fax:81-t2-778-9924)
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               JOURNAL
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30596 AAGTGTAAAT------TGGCAAGAGCACTTTGGAGACTCAGCAAGAATATCTAAAG 30646
                                                                                                                   30647 crcaaggrgcrrargrcagcacrcagcacraccarrccraacarg----racaagagg 30702
                                                                                                                                                                                                                                                                                                                                                                                                                   10823 ACAAAAAATTAATGAACCAACAAAAATTAATGTACAACAAAAGAAATTAATGAA 30882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30883 CCACAGCTAGATGTGTCATTATGAATTACTGTCAAAAACATAATGTTAAGTTAAAAAAC 30942
                                                                                                                                                                                                                                                                                                            4908 TGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAACAAAGAGGAGAGAAATCAG 4967
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Hattori,M., 1shi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fuljsama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 184,672 genomic DNA of 18412
Published Only in Database (2000)
Lases 1 to 184672)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Pujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                       TTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTATTTCCACAAATGCTATTCAAATTAG
                                                                                                                                                                                                                     4968 TCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGTTAAAAAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5088 GAAAGACTAGAGGAATAAACA-CAAGAÀTCTTAACAGTCATTGTCATTAGACACTAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5147 TAATTATTATTAGACACTATGATATTTGAGATTTAAAAAATCTTTAATATTTTAAAA
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Homo sapiens DNA, clone:RP11-873E20.
Homo sapiens
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96228 96527: gap of 700 bp 96528 103158: contig of 6631 bp in length 103159 103288: gap of 100 bp 10329 103288: gap of 100 bp 10329 103288: gap of 100 bp 10329 103288: gap of 100 bp 103691 107180: gap of 100 bp 114099 114199: contig of 6918 bp in length 114099 114199: contig of 6918 bp in length 12021 125909: contig of 5822 bp in length 120201 125909: contig of 5822 bp in length 125910 126009: gap of 100 bp 100 bp 132286: gap of 100 bp 132386: gap of 100 bp 132386: gap of 100 bp 132386: gap of 100 bp 13750 13749: gap of 100 bp 14783 145815: contig of 4842 bp in length 14732 141831: gap of 100 bp 145959: gap of 100 bp 155954 155958: contig of 2845 bp in length 145957 153443: contig of 3847 bp in length 153844 155343: contig of 2845 bp in length 153844 155953: gap of 100 bp 155889: lesses: gap of 100 bp 15589: lesses: gap of 100 bp 1558
                                                                                                       38132: gap of 100 bp
48298: contig of 10166 bp in length
48398: gap of 100 bp
58440: contig of 10042 bp in length
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100 bp
7503 bp in length
17: gap of 100 bp
26921: contig of 12504 bp in length
21: gap of 100 bp
38032: contig of 11011 bp in length
                                                                                                                                                                                                                                p of 100 bp
contig of 8991 bp in length
                                                                                                                                                                                                                                                                            p of 100 bp contig of 8402 bp in length
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62866 166636: contig of 3771 bp in length
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96427: contig of 7503 bp in
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178407: contig of 3337 bp
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169695: contig of 2959 bp
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12368 172467; gap of 100
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Matches 417; Conservative
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Zathoun, J., Zembek, L., Zimmer Direct Submission JOURNAL Submitted (20-FEB-2002) White Research, 320 Charles Street, 4 (bases 1 to 143517) AUTHORS Birren, B., Linton, L., Nusbaum Anderson, S., Barna, N., Bastie Brown, A., Camarata, J., Campop Choepel, Y., Colangelo, M., Col Cook, P., DeArellano, K., Dewa Ferreira, P., Filzhudh, W., Gag Ginde, S., Gord, S., Goyette, M.	Hagos, B., Horton, L., Hulme, W. Kamat, A., Karatas, A., Kells, C. Landers, T., Lehoczky, J., Levi Macdonald, P., Major, J., Marqu McEwan, P., Marcernan, R., Meldr Menga, V., Murphy, T., Naylor, Norman, C.H., O'Connor, T., O'D Peterson, K., Phunkhang, P., Pl Retta, R., Riebback, M., Riley, R Rosetti, M., Roy, A., Santos, R.	AL.	COMMENT On Jun 28, 2002 this sequence All repeats were identified u Smit, A F.A. & Green, P. (199 http://ftp.genome.washington	/organism="+nomo sapi. /db_xref="taxon:9606 /chromosome="17" /map="17" /clone="RP11-462C21"	repeat_region 24. 248 repeat_region 7pt_family="AluSg/x repeat_region 7pt_family="MiR" repeat_region 433, 722 repeat_region 7pt_family="MiR" repeat_region 7pt_family="AluJo" 878. 913 722 repeat_region 7pt_family="AluJb" repeat_region 7pt_family="AluJb" repeat_region 7pt_family="RIMM_C" repeat_region 7pt_family="RIMM_C" repeat_region 7pt_family="MIR"	repeat_region 32103429 /rpt_family="MIR" /rpt_family="MIR" /rpt_family="LTR33"
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Homo sapiens Homo sapiens

SOURCE

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Unpublished

I (bases 1 to 199582)

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Birren, Ba., Fagaman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Bakren, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baver, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bovon, K., Dewan, K., Donelan, L., Etemali, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Borton, L., Howland, J.C., Hull, L., Jacotcot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Morlan, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavilin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Shyam, R., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Torruella-Miller, J., Vassiliev, H., Vo, A., Wange, E., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M.
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Is Submitted (07-Adc.1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 7, 1998 this sequence version replaced #1:3399679.

All repeats were identified using Repeatmasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/Repeatmasker:html.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 198582)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone hRPR.401_0_9
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AC104520 31632 bp DNA linear PRI 01-MAY-2002
Homo sapiens chromosome 19 clone LLNLF-137B9, complete sequence.
AC104520
AC104520.2 GI:20376977
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3703 TTTCCTTACTTATTATGAATACTTAATTTCCCTTTTAATCTTTTTAGATTGCAAAAGTA 3644
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submission
Submission
Drive, Walnut Creek, CA 9498, USA
On May 1, 2002 this sequence version replaced 91:17646891.

Draft Sequence Produced by DOE Joint Genome Institute
Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu
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                                                                                                                                      12;
Quality: Phrap Quality >=40 98.3% of Sequence;
Estimated Total Number of Errors is 0.3.

NOTE: This insert is not the entire sequence of the clone. It is
clipped at the overlaps with AC053467 and AC005595. The number of
bases overlapped with AC053467 is 3566 and with AC005595 is 13219.
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                                                                                                                                                               AGGCTGAGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGC
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                                        Location/qualifiers
1. 31632
Acrganism="Homo sapiens"
Ab xref="taxon:9606"
/chromosome="19"
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                                                                                   /clone="LLNLF-137B9"
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AC053467 41407 bp DNA linear PRI 16-APR-2000 Homo sapiens chromosome 19, cosmid R28310 (LLNL-R_243G6), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-APR-2000) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Mational Laboratory, 7000 East Ave., Livermore, CA 94551, USA
28310 is separated from BAC 349488 (CIT-B-518-p12) on the left by a
gap of approximately 5 kb, and separated from cosmid F16601 on the
right by a gap of approximately 2 to 8 kb. Additional chromosome
19 map and sequence information may be obtained at:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 41407)

Lamerdin,J.E., McCready,P.M., Skowronski,E., Viswanathan,V., Burkhart-Schultz,K.J. Gordon,L., Dias,J., Ramirez,M., Stliwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J., Danganan,L., Elter,A., Christensen,M., Georgescu,A., Avila,J., Liu,S., Attix,C., Andreise,T., Trankheim,M., Gorgescu,A., Amico-Keller,G., Coeffeld,J., Duarte,S., Lucas,S., Bruce,R., Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. an Carrano,A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence analysis of a 6 Mb region in 19p13.3 between CDC34 and
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/clone_lib="LL19NC03 R chromosome 19-specific cosmid
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/map="19p13.3 between D19S883 and D19S325"
/clone="R28310"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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complement(2420. 2557)
/rpt_family="Aludb"
complement(2575. 2870)
/rpt_family="Alusx"
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/rpt_family="AluJo/FRAM"
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/rpt_family="Alux"
complement(367. 560)
/rpt_family="MER20"
1408. 1697
/rpt_family="AluSx"
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AC053467.1 GI:7577567
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Complement(3656..3678)

/rpt_family="AT_rich"

complement(4013..4378)

/rpt_family="AT_rich"

complement(4013..4374)

/rote="BLASTN similarity to AA551654 nf98ail.s1

NCI_CGAP_CO3 Homo sapiens CDNA clone IMAGE:927932 3'

(362..3); match 1.00; database searched: est"

complement(join(4546..4594,4617..4869))

/rote="BLASTN similarity to AA282079 zt04965.s1

NOT_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:712184 3'

(324..276,253..1); match 1.00; database searched: est"

complement(4959..5010)

/rpt_family="MIR".5276)

/rpt_family="MERS8A"

5303..5548
                                   /gene="ICBP90"
/product="ICBP90 transcription factor mRNA"
/note="This accession contains nt 2234-2382 of ICBP90 mRNA
                                                                                                                                                                                                                                                                                                  /translation="DCLDRSFRAQVFSCPACRYDLGRSYAMQVNQPLQTVLNQLFPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8801. .8886
//note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 62.000"
complement(9306. .9593)
                                                                                                                                                                     /note="ICBP90; putative transciptional regulator of topoisomerase IIalpha expression"
/note="Homo sapiens transcription factor ICBP90"
                                                                                                                                                                                                                                      .793"
                                                                                                                                                                                                                                 /product="ICBP90 amino acids 746.
/protein_id="AAF64067.1"
/db_xref="GI:7577568"
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complement(8320 .8603)
/rpt_family="AluJb"
8801 .8886
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:omplement'in
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/rpt_family="MIR"
complement(11984. .12273)
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6359 .6406
/rpt_family="LIMB8"
6675. .6976
/rpt_family="Alusx"
complement(6982. .7283)
/rpt_family="AluJo"
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complement(8022 R210)
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complement(5646. .5949)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="LiMB6"
complement(7372..7669)
/rpt_family="Alusx"
complement(7673..8012)
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/rpt_family="AluJb"
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                                                                                                                          <3375. .3521
/gene="ICBP90"
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                                                                                                      CDS AF129507." <33375. .3521
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/rpt_family="Alusx"
/rpt_family="Alusg"
19022...19098
/note="predicted exon, program: grail2exons_human_l.3,
frame: 2, quality: excellent, score: 87.000"
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                   complement(15172. .15334)
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complement(15508. .15565)
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firame: 0, quality: excellent, score: 99.000"
complement(15833. .15893)
                                                                                      /note="predicted exon, program: grail2exons_human_1.3, frame: 0, quality: good, score: 73.000" complement(15908. 16206)
Typt_family=Ralusx"
16462. 16547
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49.4%; Pred. No. 7.2e-37;
tive 1; Mismatches 957;
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/rpt_family="AT_rich"
complement(25330. .25628)
/rpt_family="Alusg"
complement(2552. .25847)
/rpt_family="MER33"
26791. .26909
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complement(22841. .23134)
/rpt_family="LiMB8"
complement(23146. .23445)
/rpt_family="AluSx"
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24728. .250>>
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17873. .18185
/rpt_family="MER58B"
complement(18312. .186
                                                                                                                                                                                                               /rpt_family="Alusx"
17522. .17752
                                                                                                                                              /rpt_family="L1MC1"
16566. .16832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AluSx"
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6835. .17139
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.7175. .17473
         /rpt_family="MIR" complement(15172.
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38785 GGTGAGCTGAGATCACACTGCAGCCAGCCTGGGCGACAGAGCGAGACACTGTCTAA 38726
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                            AAAAAATAAGAAGAAAAATTAAAAATAAAATGGAAACAACTACAAAGAGCTGTTGTCCTAG
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  AGCCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGC
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37957 GTGGTGCAAGGGAGATGAAAGAAGCCAGAACACAAGGAGAGGGGATGACAGGGGAGCTG 37898

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3539 TTTAAAGTGAAACAGACAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGG

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TTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACAGCACTAGCTCCAC 4730
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                                                   AAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCT
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Homo sapiens chromosome 1 clone RP11-4M23, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                     ALS90609
ALS90609.14 GI:15795484
                                                                                                                                              human.
RESULT 10
AL590609/c
                                                 DEFINITION
                                                                                                                                                            ORGANISM
                                                                                       ACCESSION
                                                                                                          VERSION
KEYWORDS
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150235
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                                                                                                                                                                        Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATCCATTTAGATTAAAATATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3474 AATCTAGTTGCTGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCATGTACGTGAGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3235 TITITIAAAAGACAATCTCACCCTGTTACCCAGGCTGGAGTGCAGTGGTGCAATCATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3295 TTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTCCCAAAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
         Direct Submission
Submitted (15-SEP-2001) Sanger Centre, Hinxton, Cambridgesna CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk
On Sep 27, 2001 this sequence version replaced gi:15787779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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63.8%; Pred. No. 6.8e-37;
ive 0; Mismatches 238;
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. 38794 c 38902 g 47961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/chromosome="1"
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(bases 1 to 171073)
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Best Local Similarity 63.88
Matches 453; Conservative
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as it is available and the accession number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252427 252256: gap of 100 bp
252527 255520: contig of 2994 bp in length
255521 255620: gap of 100 bp
255621 265239: contig of 6699 bp in length
                                                                                     3348: gap of 100 bp
178414: contig of 5066 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262320 262419; gap of 100 bp
262420 264483; contig of 2064 bp in length
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                                                    150064 ACCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTTGCCCAGCCGCC 150005
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                                                                                                                                                                                                                                                                                                                                                                                                CCTGTGGTCCCAGCTACTAGGGGGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAA 3765
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270269)
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Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21911471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5
Sequencing vector: M13: M7815; 09% of reads
Sequencing vector: M13: M7815; 09% of reads
Sequencing vector: plasmid: L08752; 99% of reads
Chemistry: Dye-terminator; 4% of reads
Chemistry: Dye-terminator; 100 Dye; 95% of reads
Chemistry: Dye-terminator; 100 Dye; 95% of reads
Consensus quality: 261411 bases at least 040
Consensus quality: 266087 bases at least 020
Insert size: 268469; sum-of-contigs
Insert size: 176357; 3.4% error; agarose-fp
Quality coverage: 10.19x in Q20 bases; sum-of-contigs Quality
coverage: 17.81x in Q20 bases; agarose-fp
                                                                                                                                                                       CTCTGGGAGGCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCA
                                                                                                                                                                                                                                                                                ACATGCCAAAACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGCATGTG
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AL590728.23 GI:22002653
HTG: HTGS_PHASEI: HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Homo sapiens.
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* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3826 GCCTCAAAAAATAAGAAGAAAATTAAAAATAAATGGAAACAACTACAA 3875
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Unpublished
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TITLE
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                                               AC025620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3652 ACATGGCAAAACCCTGTTTCT----ATAACAAAAATTAGCCGGGCATGGTGGCATGTG
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                                                                                                                                                                                                                                                                                                                                                                       Length 270269;
                                                                                                                                                                                                                                                                                                                      1807 others
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                                                                         24835. 250284
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                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 241.2; DB 2;
63.8%; Pred. No. 6.5e-37;
iive 0; Mismatches 238;
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Best Local Similarity 63.8
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27127 GGGAGACTCCGTCTAAAAACAAAACAAAACAAAACAACAGTATTGCAATGCTTAGGTGTA 27186
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                ACACAAGAATCTTAACAGTCATTGTCATTAGACACTAAGTCTAATTATTATTAGACA
                                                                                                                                                                                                                                                           27726 CCACTAGACTCTATAAGACACAGTAGGTAAACAGAATCCTTCACAATGTTTTGGTAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCATGCTGGAGTGGAATGGCATGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5403 GGTAGATGGGATTACAGGCGCCCACCACCACCACGCTAATGTTTGTATTTTAGTAGA
                                                27606 CCTTGGTACCTTTCCATGACCTCAGATTATTATCTTTGTATCATATATTCTTCAGAGTTC
                                                                                                         ATGCAATCAGTATAATCCAAATCATGTAAATATGTGCCTGTAGAAAGACTAGAGGAATAA
                                                                                                                                                                                                                                                                                                                 5166 CTATGATATTTGAGATTTAAAAATCTTTAATATTTTAAAATTTAGAGCTCTTCTATTTT
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Submitted (08-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. OM 63108, USA
On Aug 17, 2000 this sequence version replaced di:8439998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aug 17, 2000 this sequence version replaced gi:8439998
4992 AGATATTTAGATTTTGACTAGTTAAAAAAGCAGCAGAGTACAAAATC---
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AC023132.4 GI:9838192
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Waterston, R. H.
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Waterston, R.H.
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* NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                Quality coverage: 4.17 in Q20 bases; agarose-fp
Quality coverage: 4.48 in Q20 bases; sum-of-contigs
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152790: gap of unknown length
169160: contig of 16370 bp in length
169260: gap of unknown length
186107: contig of 16847 bp in length.
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9367. .101493
/note="assembly_name:Contig39"
101594. .110504
/note="assembly_name:Contig40"
110605. .123442
/note="assembly_name:Contig41"
123543. .137014
                                                                                                                                                                                                                      /note="assembly_name:Contig35"
71758 .79804
700te="assembly_name:Contig36"
7905 .87292
/note="assembly_name:Contig37"
87393 .93566
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/note="assembly_name:Contig31"
50912. .55898
/note="assembly_name:Contig32"
55999. .58369
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17875. .20600
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/note="assembly_name:Contig20"
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/note="assembly_name:Contig21"
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12678. 14655
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/note="assembly_name:Contig23"
14756. .17774
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/note="assembly_name:Contig25"
20701. .24794
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24895. .28615
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28716. .33164
/note="assembly_name:Contig28"
33265. .37827
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37928. .43629
/note="assembly_name:Contig30
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/note="assembly_name:Contig33"
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/note="assembly_name:Contig34"
64938. .71657
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152791. .169160
/note="assembly_name:Contig44"
169261. .186107
                                                                                                                                                                                          1352. .2882
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                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  .12577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_end:T7
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152791
169161
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                                                                                 Source
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99043 AAACTTTATGGTGTAAATTTTATCTCAATGCTGTTTAAAGGTAAAAGAGTAAAGGGAGT 99102
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                                                                                                                                                                                                                                                                                                                                                                                                                               99103 GTAGAGTTACCAGTTTCAATGTACATTTAACAGGAGTTTAATATAAGGAAAATGGAGATA 99162
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                                                                                                                                                                                              3286 AATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTC 3345
                                                                                                                                                                                                                                                               CCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTGGCCTAGGATC---CATTTAGA 3401
                                                                                                                                                                                                                                                                                                                            3402 TTAAAATTTTTAAATTTTAAATAATATGGCTAATTTTTACCTTATGTAATGTGT 3461
                                                                                                                                                                                                                                                                                                                                                                                               3462 ATACTGGTAATAAATCTAGTTTGC-TGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCA 3520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGGCATGTGCCTGTGGTCCCAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAG 3752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3753 CCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCTGGGTGAC 3812
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Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-1070A24
Unpublished
                                                                                                                               3226 TGTTTTTGATTTTTAAAAGACAATCTCACCCTGTTACCCAGGCTGGAGTGCAGTGGTGC
                                                                                                 Gaps
                                                               Length 186107;
                                                                                                 14;
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                 3037 others
                                                                                               Indels
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AC113194.7 GI:22417385
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                             4.4%; Score 240.4; DB 2;
66.2%; Pred. No. 9.6e-37;
tive 0; Mismatches 211;
/note="assembly_name:Contig45"
54061 a 37551 c 36981 g 54477 t
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Homo sapiens chromosome 8 clone RI
IN PROGRESS ***, 2 ordered pieces.
                                                                                               Matches 441; Conservative
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99523 AGAAAG 99528
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                                                                                Best Local Similarity
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                                                                  Query Match
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                 BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
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AC113194
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/organism="Homo saplens"
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/chromosome="8"
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/clone="RP11-1070A24"
Location/Qualiflers
                                                                                                                                                                                                                                                                                                              Matches 441; Conservative
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Homo sapiens
                                                                                                                                                                                                                                                                                        Best Local Similarity
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AC069335
  FEATURES
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    2 Intron. L. 1. 10208164)

Birran, B., Lintcon. L. Nusbaum. C., Lander, E., Ali. A., Allen, N., Anderson. S., Barna, N. Bastien, V. Boguslawkiy, L. Boukhgalter. B., Choepel. Y. Canangara. J. Campoplano, A. Chang, J. Boukhgalter. B., Choepel. Y. Calangelo. M., Canglano. R., Chang, J. B. Dodder, S., Gook, A., Concepel. Y. Calangelo. M., Canglano. R., Chang, J. B. Dodder, S., Earch. S., Eartels. P. Ertzellano. K., Landers. S., Dodder, S., Earch. S., Gooke, S., Grode, S., Goyette, M., Gage, D., Galagan, J., Gardel-Brere. N., Hulme, W., Illev, I., Johnson, R., Johnson, R., Johnson, R., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Major, J., Marquis, N., Matthews, C., McCarthy, M., Reback, M., Rileo, E., Roggov, P., Schauer, S., Schuber, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyan, D., Yew, J., Young, G., Zahoun, J., Zembek, L., Zimmer, A. and Trigilio, J., Yew, J., Young, G., Camarata, J., Chara, M., Travers, M., Travers, M., Travers, M., Travers, M., Tavers, M., Machen, J., Chazaro, B., Chopell, Y., Callymor, A., Gard, P., Conter, P., Devar, R., Lindhaller, M., Gade, D., Galagan, J., Gard, P., Callymor, A., Machen, J., Chara, T., Boukhaller, B., Cord, S., Crahaer, P., Boukhaller, M., Gade, D., Galagan, J., Matthews, C., McCarthy, M., Wallor, M., Machen, J., Matchen, J., Hulme, W., Jikey, J., Johnson, R., Johnson, R., Johnson, R., Machen, J., Machen, J., Topham, K., Travers, M., Travers, M., Velle, K., Travers, M., Velle, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the finished sequence as soon as it is available and the accession number will be preserved.

1 41535; contig of 41535 bp in length
41536 41635; gap of 100 bp
41636 208164: contig of 166529 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
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JOURNAL
REFERENCE
                        AUTHORS
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79398 ATGATGGGAAAATAACAGTTAAAAAGAAGTAGGAGCCCGGGCATGGTGGCTCATGCCTA 79457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79338 GTAGAGTTACCAGTTTCAATGTACATTTAACAGGAGTTTAATATAAGGAAAATGGAGATA 79397
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Homo sapiens BAC clone RP11-723C11 from 7, complete sequence.
ACU69335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3462 ATACTGGTAATAAATCTAGTTTGC-TGCCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCA 3520
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                                                                                                                                                                                                                                                                                                                      3286 AATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTGGCCTC
                                                                                                                                                           Indels 14; Gaps
                                                                                                      Length 208164;
                              100 others
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58228 a 41625 c 43295 g 64916 t 100
                                                                                                      4.4%; Score 240.4; DB 2;
66.2%; Pred. No. 9.5e-37;
tive 0; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC069335.17 GI:15290496
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Genomics 51:1-8. The clone may be obtained either from
                Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bepeac.med.buffalo.edu)
WECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-785H2; the clone sequenced to the right is RP4-592P3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-723C11; actual end is at base position 1 of RP11-723C11; actual end is at base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus EST AA667697 (NID:92626398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="similar to Bos taurus EST AW660583 (NID:97426410)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MERl_type"
3455. .3606
/rpt_family="MERl_type"
3662. .3850
3665. .3850
3665. .3850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG721725 (NID:914000912)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18. .264
/note="match to EST AW814659 (NID:97907653)"
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                                                                                                                                                                                                                                                      Polymorphisms exist between AC069335 and AC006452.
Location/Qualifiers
1. 155521
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(TTTTG)n"
572. .854
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2599. .2622
/rpt_family="AT_rich"
2616. .2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
1789. 1837
/rpt_family="A-rich"
1838. 1924
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-723C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-11"
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/note="similar to H.
(NID:g12345320)"
4320. .4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to EST 878. .1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        878. .1170
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1210. .1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(T)n"
2101. .2417
/rpt_family="Alu"
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805. .810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
2093. .2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
2550. .2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
4303, .4459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu"
4317. 4343
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1508. .1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu" 3237, .3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L1"
1925. .2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family-"L1"
2911. .3200
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                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 15521)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-JAM-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Aug 25, 2001 this sequence version replaced gi:13431253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1552)]
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mallto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MoD 63108, USA
5 (bases 1 to 155521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
                                                                                                                                                                                     2 (bases 1 to 155521)
Ozersky,P., Du,H. and Maupin,R.
The sequence of Homo sapiens BAC clone RP11-723C11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- Genome Center
                                                                                                                                                                                                                                                      Unpublished (2001)
3 (bases 1 to 155521)
Waterston, R.H.
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6 (bases 1 to 155521)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
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COMMENT

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14303 TTGGGAGTGAAAATATCCTCAATATTACAATGGTTTATGGCCCTCCAAAGGGCCATACAC 14362
                                                                                                                                                                                                                                         GATGAGCTACTTAGTTAGGCTGATATTTTGGTATTTAACTTTTAAAGTCAGGGTCTGTCA 3950
                                                                                                                                                           4011 GAATGTTCATAGTACCTTTATTCACAAAACCCCAAAGTAGAGACTATCCAAATATCC--A 4068
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                                                                                                                                                                                      14363 AGTACATCTGTGGTATTACATTTCATAGGCCAAGATCACTCCACTGCACTCCAGCCTGG
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                                                                                                                                                                                                                                                                                     CCTGCACTACATTATAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTACGT
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                                                                                                                                                                                                                                                                                                                        4189 CAGACATGAAGGAGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               4428 TGGGGAGGGAAGGACTGCAAAGAGGGAAGATCTGGTGGGGGTGAGGTGGTGATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4606 AAAATAATGTGTAAGAAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTGA
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                      /note="match to EST AW594046 (NID:g7281304) hg44a03.xl"
4513. .4562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGG
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Pred. No. 1.5e-36;
1; Mismatches 982;
                                                                                                                                                                                                                                                                                                              7264. .7455
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7465. .7709
/rpt_family="Alu"
7717. .7833
                                                                                                                                                                                /rpt_family="AT_rich"
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5842. 6133
6701. 6852
/rpt_family="L2"
/rpt_family="L2"
/rpt_family="C"
/rpt_family="C"
/rpt_family="C"
/rpt_family="AT_rich"
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                                       4513, .4562 /rpt_family="L1"
4566, .4626
/rpt_family="ERV1"
                                                                                           4641. .4889
/rpt_family="Alu"
4890. .5219
/rpt_family="L1"
5220. .5522
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/rpt_family="(A)n"
10396. .10669
/rpt_family="Alu"
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/rpt_family="Alu"
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8737. .9045
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                                                                                                     15439 ATTGGTGGTTAGCAGGGGCGGAGGACCGGGGGTGGTGAGAGTTATAAAGGAATAGCATGA 15498
                                                                                                                                 5070 TGTAAATATGTGCCTGTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTG 5129
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               4950 AAGAGGAGGAGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTT
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SS			Description	Human activation-i	Human activation-i	Human cDNA differe	Human musculoskele	Human cDNA differe	Human immune/haema	Human digestive sy	Genomic sequence #	Human digestive sv
SUMMARIES			ID	AAC55313	AAC55339	ABK83567	AAL35901	ABK83567	AAK80162	AAK89461	AAS39620	AAK89019
			DB	21	21	24	22	24	22	22	22	22
			Match Length DB ID	5514	11204	112460	28818	112460	4126	4126	32204	32204
	ф	Query		100.0	89.3	4.2	4.2	4.1	4.1	4.1	4.1	4.1
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ALIGNMENTS

RESU AAC5 ID XX AC	RESULT 1 AAC55313 ID AAC55313 standard; DNA; 5514 BP. XX AC AAC55313;	
X E X	05-FEB-2001 (first entry)	
DE XX	Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:9.	
K	Activation induced cytidine deaminase; AID; cytidine deaminase;	
X X	immune related disease; allergy; allergic disease; antiallergic;	
K	direction. dene therapy: B cell associated immune system disorder; food allergy;	
ΚW	immunodeficiency disease; immunoglobulin A deficiency disease; asthma;	
ΚM	IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;	
ΚW	drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;	
ΚW	ataxia telangiectasia; common variable immunodeficiency disorder;	
ΚW	major histocompatibility class II deficiency disease;	
X X	auto immunodeficiency syndrome; IgG subclass selection disorder; ds.	
XX		
S ×	Homo sapiens,	
PN	WO200058480-A1.	
XX DA	05-OCT-2000.	
X		
PF	28-MAR-2000; 2000WO-JP01918.	
X		
PR		
PR		
ጸፈ	27-DEC-1999; 99JP-0371382.	

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protein may be used for diagnosis and treatment of these disorders. The
                                                      as
                                                      on induced cytidine deaminase, useful for immune-related diseases including
                                                                                                                                                                                                    sequence represents a genomic DNA sequence of human AID.
                                                                                            present invention describes an activation-induced cytidine
                                                     ding activation induced development for immune-
                                                                              Claim 17; Page 142-145; 174pp; Japanese.
                           Ξ
                                                    encoding
       TOBACCO
                         Honjo T, Muramatsu
                                       WPI; 2000-611715/58
                                                           drug
      JAPAN
                                                            for
                                                    Nucleic acid
                                                                  allergies -
                                                            target
      (NISB)
(HONJ/)
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Q Sequence 5514 BP; 1709 A; 1045 C; 1134 G; 1623 T; 3 other;
Query Match
Bost Local Similarity 100.0%; Pred. No. 0;
Matches 5514; Conservative 0; Mismatches 0; Indels 0; Gaps

ö 240 420 480 540 GTATCAAAGGCTTGAGGCAGGAAGAGAGCAGAGCCCTAGCTGCATTGCTTAGCATTGCA 120 420 9 TCCCTAGCACCTGGCATAGTTTCCATTAACAGTAGGCATGAAGTATCTACTCAGTGAATA ACAGACGAATACATGGTCCAAGCTAGGGCTATTGATTTGAAAATCATCAAGGTATAGATG TATGAGAGCACAAAATTAAAGTCTTTTATTTGAAGATCTTAGCCTGTTTTCCAAATTCAG TGCAGCCAGTTAGACACTGATTCTGTCTGGTGAAACAAGCATTTTTGTATTTTGGGGGAC CAAAAATCACTCTTTGGTGTAAATATCTAGTCTTCAAGCAATTCTTGTAATGCAATCAGA **AAGAAAAAAA**TCCATGGTTTGGGAGGCAAAATTTTTGTGTTCTAAATTCTATATAACTGA ~ 61 61 121 121 181 181 301 301 361 361 421 121 481 481 g à à g ð g g g õ ç Q B ò g ò q ò

1080 1200 1200 1260 1020 1020 1080 1260 1320 1380 1500 1620 900 900 099 720 780 780 840 840 900 900 960 960 9 720 TAGCTATGGAGCATGGGCTTTTAGAGCAGCAGCCCCAAAGGAACCTAAACATTAA CATCTTCACTGGATCCAAATCAGGAGCAAGGCCGTTGGGGTACCTGGTGGGGGTGATGCT GTCAGGGGAGGCCCAAAAGGGCCAAGCTCAAATTTGAATGTGAAGGCCCAATGCACTGT GGGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAGTCTTCTCGTG GGGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAGTCTTCTCGTG GGTGATTGCACTGGCCTTCCTCAGAGCAAATCTGAGTAATGAGACTGGTAGCTATCCC AGACTGTGGGAATATGGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACACAAATAACCCAA TATTTTGTGTTATCATGATTATAATTGAAGTGTCTACTGTTACTGCCTCCTGATCTTTGC GTCAGGGGAGGAGCCCAAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCCAATGCACTGT TTTCTCTCATGTAACTGTCTGACTGATAAGATCAGCTTGATCAATATGCATATATTTT TTCAGACTTCTCTTGATTTCCCTCTTTTTCATGTGGCAAAAGAAGTAGTGCGTACAATGT ACTGATTCGTCCTGAGATTTGTACCATGGTTGAAACTAATTTATGGTAATAATAACA TAGCAAATCTTTAGAGACTCAAAATCATGAAAAGGTAATAGCAGTACTGTACTAAAAACGG TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA TAGTGCTAATTTTCGTAATAATTTTGTAAATATTCAACAGTAAAACAACTTGAAGACACA CTTTCCTAGGGAGGCGTTACTGAAATAATTTAGCTATAGTAAGAAAATTTGTAATTTTAG 841 1021 1021 1081 1081 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 601 199 661 721 721 781 781 901 901 961 961 Op ò g ò g ŏ q ò g ò QQ ŏ g Ωý qq οy g οy g δ g οy Ω ò Db ò QQ ò Db ŏ pp οy qq qq

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46 66 66	g d do d	da da da	QY Db	Db Oy	oy Oy	do oy	da o	do oy	yo da	o da da
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qa	3781 TGC	CTIGCGCCACIGCACICCAGCCIGGGIGACAGGACCAGACCTIGCCICAAAAAAAAA 3840	•		
Qy	3841 GAZ	GAAAAATTAAAAATAAAATGGAAACAACTACAAAGAGCTGTTGTCCTAGATGAGCTAC 3900	4	921 CAAGACACTGTGCTA	- C-
q	3841 GA	GAAGAAAATTAAAAATAAATGGAAACAACTACAAAGAGCTGTTGTCCTAGATGAGCTAC 3900	4		I GC I'A
ογ	3901 TTR	AGTTAGGCTGAFATTTTGGTATTTAACTTTTTAAAGTCAGGGTCTGTCACCTGCACTAC 3960	oy 4	981 ACAACATAGCAAGAT	AAGAT
qa	3901 TT	GTTAGGCTGATATTTTGGTATTTAACTTTTAAAGTCAGGGTCTGTCACCTGCACCTAC 3960	er L		MAGAI
Οy	3961 AT	TATTAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTACGTGAATGTTCAT 4020		5041 CACACATGCAATCAG	P. C. A.C.
qq	3961 ATT	ATTAAAATTCTCAATGTATATCCACACAAAAGACTGGTACGTGAATGTTCAT 4020		5041 CACACATGCAA	ביייט ביי
Ολ	4021 AG	AGTACCTTTATTCACAAAACCCCAAAGTAGAGACTATCCAAATATCCATCAACAAGTGAA 4080	y g	5101 AATAACACAAGAAT 	
qq	4021 AG	ACCTITATICACAAAACCCCAAAGTAGAGACTAICCAAATAICCAICAAGAGIGAA 4080			
Qy	4081 CA	CAAATAAACAAAATGTGCTATATCCATGCAATGGAATACCACCCTGCAGTACAAAGGAAG 4140		5161 AGACACIAIGAIA11 	
qq	4081 CA	NATAAACAAAATGTGCTATATCCATGCAATGGAATACCACCTGCAGTACAAAGGAAG 4140		Sign Addition	
Qy	4141 AAC	AAGCTACTTGGGGATGAATCCCAAAGTCATGACGCTAAATGAAAGGGTCAGACGTGAAGG 4200		5221 AIIIIICCAIAGIAI 	
QQ	4141 AAG	CTACTTGGGGATGAATCCCAAAGTCATGACGCTAAATGAAGAGTCAGACATGAAGG 4200		5281 THTTTTTTTT	A DILL
ΟY		AGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTATAGTTACAGAAA 4260		5281 THEFT THEFT S	11111
qa	4201 AGG	GAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTATAGTTACAGAAA 4260		5201 1111111111	
Qy	4261 GC7	GCAAATCAGGGCAGGCATAGAGGCTCACACCTGTAATCCCAGCACTTTGAGAGGCCACGT 4320	à á	0341 AICAIAGCICACIGC	
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Ολ	4321 GGC	GGGAAGATTGCTAGAACTCCAGGAGTTCAAGACCAGCCTGGGCAACACACAGTGAAACTCCAT 4380		5401 CGGGTAGATGGGATT	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
q	4321 GG	SAAGATTGCTAGAACTCAGGAGTTCAAGACCAGCCTGGGCAACACAGTGAAACTCCAT 4380		SAUL CGGGIAGAIGG	TASS
ογ	4381 TC1	CCACAAAAATGGGAAAAAAAAAAGAAATCAGTGGTTGTCCTGTGGGGAGGGGAAG 4440		5451 GAGATGGGGTTTCAC	
q _Q	4381 TC1	TCTCCACAAAAATGGGAAAAAAAAAAGAAATCAGTGGTTGTCCTGTGGGGGGGG	c 20	5461 GAGATGGGTT) LICHO
δy	4441 GAC	4441 GACTGCAAAGAAGGAAGAAGCTCTGGTGGTGGTGGTGATTCAGGTTCTGTATCCT 4500	RESULT 2		
qq	4441 GAC	TGCAAAGAGGGAAGAAGCTCTGGTGGGTGGTGGTGTTCAGGTTCTGTATCCT 4500	CS	5339 standard; D	DNA;
Qy	4501 GAC	GACTGTGGTAGCAGTTTGGGGTGTTTACATCCAAAATATTGGTAGAATTATGCATCTTA 4560	AAC5	5339;	
qa	4501 GAC	TGTGGTAGCAGTTTGGGGTGTTTACATCCAAAAATATTCGTAGAATTATGCATCTTA 4560	05	-FEB-2001 (first	entr
οy	4561 AA	4561 AATGGGTGGAGTTTACTGTATGTAAATTATACCTCAATGTAAGAAAAAATAATGTGTAAG 4620		activation-induced	duced
Q	4561 AA	GGGTGGAGTTTACTGTATATATACCTCAATGTAAGAAAAATAATGTGTAAG 4620		ation-induced c e related disea	cytid
Oy	4621 AA	4621 AAAAGTITCAATICTCTIGCCAGCAAACGTIATICAAATICCTGAGCCCTTTACTTCGCA 4680		naemic; antiast	thmat
qa	4621 AA	AGTITCAATICTCTTGCCAGCAAAGGTTATTCAAATTCCTGAGCCCTTTACTTGGCA 4680		cherapy; B cert odeficiency dis	sease
Qy	4681 AAT	TCTCTGCACTTCTGCCCCGTACCATTAGGTGACAGCACTAGCTCCACAAATTGGATA 4740		ephritis; gamma allergy; allerg	a-glo gic r
qa	4681 AAT	4681 AATTCTCTGCACTTCTGCCCGTACCATTAGGTGACAGCACTAGCTCCACAATTGGATA 4740		ataxia telangiectasia; c major histocompatibility	ia; c
Qy	4741 AA	4741 AATGCATTTCTGGAAAAGACTAGGGACAAAATCCAGGCATCACTTGTGCTTTCATATCAA 4800		minunoder rerene	λ λ
qa	4741 AAT	GCATITCIGGAAAAGACIAGGGACAAAAICCAGGCAICACTIGIGITTTCAIAICAA 4800	10000	2 4	
λo	4801 CC	4801 CCACGCTGTACACCTTGTGTTGTGTCTCCAGCTGCAATGGGGACTCTTGATTTCTTTAA 4860	XX PD 05-0CT	2000.	
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                                                                                                                                                                                                                                                                                                                                                                                                                       is allergy; allergic disease; antiallergic; atic; ophthalmological; anti-HIV; dermacological; ascociated immune system disorder; food allergy; sse; immunoglobulin A deficiency disease; asthma; lobulinaemia; atopic dermatitis; allergic colitis; chinitis; Rosen disease; Diceorge disease; AIDS; common variable immunodeficiency disorder; ty class II deficiency disease; syndrome; IgG subclass selection disorder; ds.
                                                   3AGATGGAGTTTTGGTCTTGTTGCCCATGCTGGAGTGGAATGGCATG
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The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antiasthmatic, ophthalmological, anti-HIV and dermacological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen immunodeficiency disorder, MIC (major histocompatibility class) class if deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and IgG subclass selection disorder. The DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID.
                                                                                                                                                                                                    as
                                                                                                                                                                                               Nucleic acid encoding activation induced cytidine deaminase, useful a target for drug development for immune-related diseases including allergies -
                                                                                                                                                                                                                                                                                        Claim 17; Page 163-170; 174pp; Japanese.
                                          (NISB ) JAPAN TOBACCO INC (HONJ/) HONJO T.
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                                                                                                         Honjo T, Muramatsu
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DB 21; Length 11204; Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 other;

1070 1130 1010 ö 710 420 480 770 180 09 AGGTTCAGAGAGACTGTGGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC **AATAA**CCCA**A**GAAGCTATTTAAATGCTCTTTAAGGTATTTACATAAATATTACTCTC CCCACCCACCCATCTTCACTGGATCCAAATCAGGAGCAAGGCCGTTGGGGTACCTGGTGG GGGTGATGCTGTCAGGGGAGGAGCCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC GAGACTTGCAGGGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAG ATTGTGCTTTTATTTTGTGTTTATCATGATTATAATTGAAGTGTCTACTGTTACTGCCTCC TGATCTTTGCTAGCTATGGAGCATGGACTGGGCTTTTAGAGCAGCCCCCAAAGGAACC TGATCTTTGCTAGCTAGGAGCATGGACTGGGCTTTTAGAGCAGCAGCCCCAAAGGAACC CCCACCCACCTTCACTGGATCCAAATCAGGAGCAAGGCCGTTGGGGTACCTGGTGG Gaps ; 0 0; Indels Query Match 89.3%; Score 4922.8; Best Local Similarity 99.9%; Pred. No. 0; Matches 4921; Conservative 3; Mismatches 591 1011 1071 551 241 361 121 771 181 891 301 421 61 951 ò g ò a ò a ò a õ g ò g ò 8 ò

1910 1500 2150 1430 1550 1670 1730 1140 1790 1260 1310 1370 1490 1250 540 720 780 840 900 960 AGAATAAAGATTTTTTAAAAATATATTTTTTTTTTAGAGACAGGGTCTTAGCCCAGCCGAG AGAATAAAGGTTTTTTAAAAATATTTTTTTTTTGTAGAGACAGGGTCTTAGCCCAGCCGAG GCTGGTCTCTAAGTCCTGGCCCAAGCGATCCTCTGCCTGGCCTCCTAAAAGTGCTGGAA TGTTCTTCAGAAAATTTTCTTGAGGTCAGACAATGTCAAATGTCTCCTCAGTTTACACTG TTATAGACATGAGCCATCACATCCAATATACAGAATAAAAGATTTTAATGGAGGATTTAA GAGACTTGCAGGGAGGCAAGAAGACACTCTGGACACCACTATGGACAGGTAAAGAGGCAG TATATATTTTTGATCTGTCTCTTTTTTTTTTCAGATCTTATACGCTGTCAGCCCCAA CGTACAATGTACTGATTCGTCCTGAGATTTGTACCATGGTTGAAACTAATTTATGGTAAT **AATATTAACATAGCAAATCTTTAGAGACTCAAATCATGAAAAGGTAATAGCAGTACTGTA** TGAAGACACACTTTCCTAGGGAGGCGTTACTGAAATAATTTAGCTATAGTAAGAAAATTT TGAAGACACACTTTCCTAGGGAGGCGTTACTGAAATAATTTAGCTATAGTAAGAAATTT GTAATTTTAGAAATGCCAAGCATTCTAAATTAATTGCTTGAAAGTCACTATGATTGTGTC CATTATAAGGAGACAAATTCATTCAAGCAAGTTATTTAATGTTAAAGGCCCAATTGTTAG GCAGTTAATGGCACTTTTACTATTAACTAATCTTTCCATTTGTTCAGACGTAGCTTAACT 1141 GCAGTTAATGGCACTTTTACTATTAACTAATCTTTCCATTTGTTCAGACGTAGCTTAACT TACCTCTTAGGTGTGAATTTGGTTAAGGTCCTCATAATGTCTTTATGTGCAGTTTTTGAT TCTTCTCGTGGGTGATTGCACTGGCCTTCCTCAGAGCAAATCTGAGTAATGAGACTGG 1911 1441 1561 1731 1791 1851 1261 1321 1971 2031 1501 2151 1371 1431 2091 1251 721 781 841 1491 1551 961 1671 1201 1381 901 Dp q g ò q δ g ò Dp ò q ΟŽ qq ð d δ qq δ g Dp g οy g δλ q δy δý δ 셤 ò δλ ò οý g ρ В

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by the appearance of grant in the specification, and comparing the expression level to an expression level in an unactivated of GCA.

The included are modulating (M2) GA by contacting of with an agent that alters the expression of at least one gene in GS; (2) screening (M3) of or an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the conformation in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of inflammation; the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile of response in a subject, exposure of a subject to a pathogen or sterile cor response in a subject, exposure of a subject to a pathogen or sterile cor response in a subject, exposure of a subject to a pathogen or sterile
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of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states
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          glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, adult respiratory distress syndrome, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is sequence represents agene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part form but the printed specification, but was obtained in electronic
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                                                                                                                                                                                              Sequence 112460 BP; 24087 A; 29523 C; 31203 G; 27647 T; 0 other;
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inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
                                                                                                                                                                                                                                                          0; Mismatches 284; Indels
                                                                                                                                                                                                                                          Pred. No. 1.5e-29;
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antilnflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                  Human musculoskeletal system related polynucleotide SEQ ID NO 2266
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PR 01-DEC-2000; 2000US-0250190.

PR 01-DEC-2000; 2000US-0250190.

PR 05-DEC-2000; 2000US-0250190.

PR 05-DEC-2000; 2000US-0255190.

PR 05-DEC-2000; 2000US-0255190.

PR 05-DEC-2000; 2000US-025186.

PR 05-DEC-2000; 2000US-025186.

PR 06-DEC-2000; 200US-025186.

PR 06-DEC-2000; 200US-02518.

PR 06-DEC
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20143 TTAATTATTTATTTTATTCTTATTTTTTTGAGACAGAGTCTCGCTCTGTTGCCCAA 20084 15; 3268 GCTGGA-GTGCAGTGGTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCA 3326 3327 ATCCTCCTGCCTTGGCCTCCCAAAGTGTTGGGATACAGTCATGAGCCACTGCATCTGGCC 3386 3428 ATAATATGGCTAATTTTTACCTTATGTAATGTGTATACTGGTAATAAATCTAGTTTGCTG 3487 3208 TFCATTTTATGTTTTTATGTTTTTGATTTTTTAAAAGACAATCTCACCCTGTTACCCAG -----GGATCCATTTAGATTAAAATATGCATTTTAAATTTTAAA 19963 AATTTTTTGTATTTTAGTAGAGGGGGTTTCACCATGTTAGCCAGGTGCCTTGGCCTC Score 230.2; DB 22; Length 28818; Pred. No. 2.4e-29; 1; Mismatches 1104; Indels 125; Gaps 4.2%; Best Local Similarity 48.7 Matches 1167; Conservative 3387 TA----20023 Query Match qq ò Op q ò ò qq ò δ 19903 CCCAAGTGCTGGGATTACAGGTGTGTGCAACCGCACCCAGCCTACAGATGATATTATAT 19844

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18974 AAAACCGTGTCTCTACTAAAATACAAAATTAGCTGGGCCCTGGTGGCACACCTGTAG 18915
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                                            19843 AATAATGAAATAGGGAAAGCTTTTCTAAGCCTACTTTCCAAATCGGAAACCAAAAAAA 19784
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CCTAAAGTTTAAAGTGCTTTCCAATAAGCTTCATGTACGTGAGGGGAGACATTTAAAGTG 3547
                                                                                                                         19603 TCCCAGCTACTTGGGAGGTTGGGGCAGGAGATTGCTTGAAGCCAGGAGTCAGAGGTTGC
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18675 GGCGCAATCTCAGCTCACTGCAACCTCCACCTCCTGGTTCAAGCAATTCTCCTGCCTCA 17896 18554 AATIGAAAICAAAAAICIAAIACIGGGAAIIGGIIACAIAAAIAIGCCACAIICAIAI 18495 18434 TCACACIATTCTGTCACATACAGGGTACAAACAATATAGTATGGTATGATACCTTTTGAAT 18375 18076 GCCTCCCGGGGTAGATGGGATTACAGGCGCCCACCACCACACTCGGCTAATGTTTGTATTT 5454 TTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAACTCCTGACCTCA 5511 18254 -TCCAAGITITCTTAAAAAGCCTGTATTCTTTTTACATTTGGGGGTCAAGGCTTGTTTTT GGCATGAYCATAGCTCCACTCCACCTCCTGGGTTCAAGCAAAGCTGTGGCTCAA 4548 ATTATGCATCTTAAATGGGTGGAGTTTACTGTATGTAAATTATACCTCAATGTAAGAAAA 8614 CTAAAGAAATAATCAGAGATTGCATAAAGATACATTATATAAGAATCGTAATACCAAAAA 18494 GATGGAAAAGTATGCAGCTACTAAAATTATGACATGCAAGAATATTGACATGGAAAAGTG TCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAAACAAAGAGGAGG 8314 TCTTTACATAGTGGGGTTATGGGTAATATAAATGTTTATTCTTTGGGCTCTTCTATCTTT **ACTAAGTCTAATTATTATTAGACACTATGATATTTGAGATTTAAAAAAATCTTTAATA** TTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCCATGCTGGAGTGGAAT 18674 TCAATTTGGAAAATTGTATAAGCCCTTTTAACAGAGTAATTACACTTGTAGACATTTTTC 4780 TCACTIGIGCITTCAIATCAACCACGCIGIACACCTIGIGCTGTCTGCAGCTGCAAT GGGGACTCTTGATTTCTTTAAGGAAACT-TGGGTTACCAGAGTATTTCCACAAATGCTAT 4959 AGAAATCAGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGTTA 5019 AAAAAGCAGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAATAT GTGCCTGTAGAAAGACTAGAGGAATAAACACAAGAATCTTAACAGTCATTGTCATTAGAC TITTAAAAITTAGAGCTCTTCTATTTTCCATAGTATTCAAGTTTGACA--------ATGATCAAGTATTACTCTTTCTTTTT .8794 AAAAAGAAAAAAAAAAAATGTAAACTATATGCCAAAATATTAAAAGTTTAACTGT 4608 AATAATGTGTAAGAAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAAATTCCTGAGC CCTTTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACAGCACTAGCTC 4728 CACAAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAA-----TCCAGGCA 4899 5079 5139 18195 5199 18135 5275 5335 5395 5455 17955 4668 5248 18075 Q QY Db δλ g Qy δy qq ογ Dp οy qq Óγ g ŏ QQ φ Q g òγ g ÓΥ q ò q QY a Ωý g δ δλ

RESULT 5 ABK83567/c ID ABK83567 standard; cDNA; 112460 XX

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The invention relates to detecting (MI) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC CDNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated CC that calters the expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent CA contact an agent capable of modulating GA or an inflammation (especially CA contacting in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the CA chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the capable of expression of the gene is indicative of inflammation; contacting the contacting contacting the contacting contacting at tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, contacting at tissue having contacting an inflammation in a tissue, and is useful for detecting GA, M2 is useful for modulating GA, M3 is useful for screening an allergic response in a tissue, M4 is useful for resonner or a sterile of resonner or a subject to a pathogen or sterile contacting an inflammation in a tissue, M4 is useful for resonner or a sterile of a subject to a pathogen or sterile of a subject to a pathogen or sterile of a subject to a subject to a pathogen or sterile of a subject to a subject to a sterile of a subject to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                                                                                                                                                                                     viral infection, parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory stress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                       Human cDNA differentially expressed in granulocytic cells #138
                                                                                                                                                                 granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vockley J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 138; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM,
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                                                      (first entry)
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                                                   14-AUG-2002
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                                                                                                                                                                 Human; ss;
ABK83567;
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95982 ACACACCACCACACCTAGCTAA-----TTTTTTGTACTTTTTGTAGAGACGGGGTTTC 95930
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                                                                                                                                                                                                                                                                                                                                                        ATGAGCCACTGCATCTGGCCTAGGATCCATTTAGATTAAAATATGCATTTTAAATTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34974.
                                                                                                      Gaps
                                                                   DB 24; Length 112460;
                                Sequence 112460 BP; 24087 A; 29523 C; 31203 G; 27647 T; 0 other;
                                                                                                    16;
                                                                                    62.7%; Pred. No. 6.6e-29;
Live 0; Mismatches 237; Indels
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ftp.wipo.int/pub/published_pct_sequences.
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                                                                     4.18;
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                                                                                    st_Local Similarity 62.7
tches 426; Conservative
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2000US-0249229
2000US-024920
2000US-0251030
2000US-0251030
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29-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
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17 - NOV - 2000;
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     31-JAN-2000; 2000US-0179065.

24-FEB-2000; 2000US-0180628.

24-FEB-2000; 2000US-0180654.

25-MAR-2000; 2000US-0180874.

16-MAR-2000; 2000US-0180874.

17-MAR-2000; 2000US-0180874.

18-MAY-2000; 2000US-0205515.

28-JUN-2000; 2000US-0205515.

28-JUN-2000; 2000US-021135.

29-JUN-2000; 2000US-021135.

30-JUN-2000; 2000US-021886.

11-JUL-2000; 2000US-0211487.

11-JUL-2000; 2000US-0225511.

14-AUG-2000; 2000US-022511.

14-AUG-2000; 2000US-022511.

14-AUG-2000; 2000US-022511.

14-AUG-2000; 2000US-022511.

14-AUG-2000; 2000US-022511.

14-AUG-2000; 2000US-022511.

15-EEP-2000; 2000US-022511.

16-SEP-2000; 2000US-022511.

17-SEP-2000; 2000US-022511.

18-SEP-2000; 2000US-02291.

18-SEP-2000; 2000US-02291.

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18-SEP-2000; 2000US-0231.

18-SEP-
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2000US-0231414
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2000US-0233063
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08-SEP-2000;
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                                                                                                                                      AAK89461;
                                                                     RESULT
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                                                                                                      AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
conclusorides may be used to produce the secreted (I), by inscrting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCTTGGCCTCCCAAAGTGTTGGGATACAGTCATGAGCCACTGCATCTGGCCTAGGAT
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                                                                                               Disclosure; SEQ ID NO 34974; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%; Score 227.6; DB 22; Length 4126; 55.2%; Pred. No. 5.8e-29; Ive 0; Mismatches 204; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4126 BP; 1237 A; 760 C; 851 G; 1278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 65.2%;
les 421; Conservative
                                 Nucleic acids encoding useful for preventing, metastasis -
WPI; 2001-483426/52
                                                                   metastasis
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Human, digestive system antigen, gene therapy; cancer, appendicitis; ulcerative colitis; infection; Hirschsprung's disease, chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
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AAK89461/c
ID AAK89461 standard; DNA; 4126
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2000US-0224519.
2000US-022513.
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2000US-0190076
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17-MAR-2000;
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19-MAY-2000;
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28-JUN-2000;
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2000US-0246609.
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2000US-0232397.
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08 - SEP - 2000 | 08 - SEP - 2
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3213 TTTATGTTTTTATGTTTTTTGATTTTTTAAAAGACAATCTCACCCTGTTACCCAGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4126 BP; 1237 A; 760 C; 851 G; 1278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3037; 986pp; English
                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC, Ruben SM;
           20000S-0249299.
20000S-0259300.
20000S-0250391.
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20000S-0251030.
20000S-0251868.
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20000S-0249297
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Matches 421; Conservative
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         17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
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GAGCCACTGCACCTGCCTATATTTTAATTAAATAAAAGTTTCAGCTGGCGTGGTGGCT

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3393 CCATTTAGATTAAAATATGCATTTTAAATTTTAAAATAATATGGCTAATTTTACCTTAT

1510 CTTTTTTTTTTTTTTTTTTTTAAATAGGGACAGGATCTCCCTATGTTGCTCCAGCT

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3453 GTAATGTGTATACTGGTAATAAATCTAGTTTGCTGCCTAAAGTTTTAAAGTGCTTTCCAAT

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25- SEP - 2000;
26- SEP - 2000;
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   1279 TTCGAGGCCAGCCTGACCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATAG 1220
                                                                                         3746 TTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; congenital abnormality; infection; colitis; inflammatory bowel disease; IBD; neoplastic disorder; gene therapy; intestinal inflammatory disorder; malabsorption syndrome; gastric; sigmoid disease; antibacterial; antiviral; antinflammatory;
                                                                                                                                                                                                                                                                                                                                                               Genomic sequence #39 encoding human colon associated polypeptide
                                                                                                                                                        3806 GGGTGACAGGACCAGACCTTGCCTCAAAAAAATAAGAAGAAAATT 3851
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AAS39620/c
ID AAS39620 standard; DNA; 32204 BP
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2000US-0215135
2000US-021647
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                                                                                  AAATAAGAAGAAAATTAAAATTAAATGGAAACAACTACAAAGAGCTGTTGTCCTAGATG
                                                                                                                                                                                                                                                                       3895 AGCTACTTAGTTAGGCTGA----TATTTTGGTATTTAACTTTTAAAGTCAGGGTCTGTC
                                                                                                                                                                                                                                                                                                      18433 TGTAATACAGCACTATGGAAGGCTGAGGCAGGAGGATTGCTTAAGCCCTAGAGTTCAAGA
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ACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCTCTC
                                 3950 ACCTGCACTACATTATAAAATATCAAATTCTCAAATGTATATCCACACAAAGACTGGTACG
                                                                                                                                                                                                                                                                                                                                                                         8373 CCAGACTGGGCAATGTAGTGAGCCCCCCATCTCTACAGGAAACAATAAAATACAATAA
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIDO at ftp. wipo.int/pub/published_pct_sequences.
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48.8%; Pred. No. 8.9e-29;
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                                               CCAGGCATCACTTGTGCT-TTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCA 4831
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18373 CCAGACTGGGCAATGTAGTGAACCCCCCCATCTCTACAGGAAACAATAAAATACAATAA 18314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4070 CAACAAGTGAACAAATAAACAAAATGTGCTATATCCATGCAATGGAATACCACCCTGCAG
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                                                                                                                               The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendictiis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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                       Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases .
                                                                                                                                                                                                                                                                                                                      DB 22; Length 32204;
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48.8%; Pred. No. 8.9e-29;
tive 0; Mismatches 967; Indels
                                                                                                  Disclosure; SEQ ID NO 2595; 986pp; English
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Matches 976; Conservative
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3662 ACCCTGTTTCT-----ATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGTGGTCC
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HUMA-) HUMAN GENOME SCI INC

S Ruben Rosen CA, Barash SC,

WPI; 2001-457727/49.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID NO: 327; 522pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

O × 8	at ftp.wipo.int/pub/published_pct_sequences. Sequence 32204 BP; 8487 A; 7076 C; 7452 G; 9189 T; 0 other;	 Db 14372 GCAGT	
n Ö	tch 4.1%; Score 226.8; DB 22; Length 32204; al Similarity 48.8%; Pred. No. 8.9e-29;	Oy 4545 AGAATT Db 14432 CAAAA	agaattatgcatcttaaatgggtgggtttactgtatgtgtaaattatacctcaatgtaaga 4604
Ma Qy	Matches 976; Conservative 0; Mismatches 967; Indels 59; Gaps 11; 3542 AAAGTGAAACAGACAGGTGGTGGTGGTCACGCCTGTAATCCCAGCACTCTGGGAGG 3601	Qy 4605 AAAAA1 Db 14492 TGTGTJ	AAAAATAATGIGIAAGAAAAGITICAAITCICITGCCAGCAAACGITAITCAAAITCCIG 4664 IGAAAAATGIGIAGAAAAAGAAAAAAAAAAAAAAAAAAA
do cy		4665	
d y	CCAAGACCGGTGGATCACCTGAGGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAA ACCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGGGTCC		TGACAGCACTAGCTCCACAAATTGGATAAATGCATTTCTGGAAAAGACTAGGGACAAAAT 4772
G &	ACCIOSTOTER TRABANTACAMAMATTAGCIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 4773 CCAGGC Db 14672 TCACTC	CCAGGCATCACTTGTGCT-TTCATATCAACCACGCTGTACCGCTTGTGTTGCTGTCTGCA 4831
9 & t	3775 GAGCAGTGCTTGCGCCACTGGGCAGGGCTGCCCCGGGGGGGG	Qy 4832 GCTGC/ 1 Db 14732 ACCCC	GCTGCAATGGGGACTCTTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTATTTCCACAA 4891
g o	AMATAAGAAGAAAAATAAAAATAGAAACAACTAGAAAAAAGAAGAGCTGTTGTCCCAGAAAAAAAA	Qy 4892 ATGCTF Db 14792 CTGCTG	ATGCTATTCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAAACAAA 4951
δ	AGCTACTTAGTTAGGCTGATATTTTGGTATTTAACTTTTAAAGTCAGGGTCTGTC	Qy 4952 GAGGAC 	GAGGAGGAGAAATCACTTATGTGGGAACAACATAGCAAGATATTTAGATCATTTGA 5011
8 8 8	TGTAATACAGCACTATGGAAGGCTGAGGCAGGAGGATTGCTTAAGCCCTAGAGGTCCAGA ACCTGCACTACATTATTAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTACG	Qy 5012 CTAGT: Db 14888 TTATT	CTAGTTAAAAAAGCAGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAATCATG 5071
d v	TGAATGTTCATAGTACTTTATTCACAAAACCCCCATCTCTACAAAAAAAA	Qy 5072 TAAAT! Db 14948 CATAG!	TAAATATGIGCCTGTAGAAAAGACTAGGAATAAACACAAGAATCTTAACAGTCATTGTC 5131
සී ඊ සි	13892 AAATGGCAGTTTCTCAGTTTGCTGTGCTGGGTTCTATGTGGGTCACTGTCTCTTCAGAATC 13951 4070 CAACAAGTGAACAAAACAAAATGTGCTATATCCATGCAATGGAATACCACCCTGCAG 4129 13952 ACTGATGGCCAGGTTCACTCTTCAAGACTGGAAGCACACAAGATGGGAATTTCA	Qy 5132 ATTAG! Db 15006 ATGAT	ATTAGACACTAAGTCTAATTATTATTAGACACTATGATATTGAGATTTAAAAATC 5191
ko d	TACAAAGGAAGAAGAAGGATGTGGGGATGAATCCCAAAGTCATGACGTAAATGAAAGGGTC	Qy 5192 TTTAA: Db 15066 ACCTC	TITAATAITITAAAATTTAGAGCICTICTATITITCCATAGTATCAAGITTGAGTAGGA 5251
8 6 6	4190 AGACCAGAACTCCAGGTATTTTTTTTTTTTTTAATTTTAAAATTATACAGGGGCCAAGC 140/1 4190 AGACATGAAGGAGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAACTTAT 4249 14072 ACGCGCCCTAAAAAATAAAAAAAAAAAAAAAAAAAAAAA	Qy 5252 TCAAG Db 15126 AAAGA	TCAAGTATTACTCTTTTTTTTTTTTTTTTTTTTTTTTTT
3 8	ACGATACAGCATCATCAGGCAGCATAGATTGGGAAACAGAACACAGAACAGAACAGAATTCAGGCAGG	Qy 5312 TGTTG(Db 15186 TGTTG	TGTTGCCCATGCTGGAGTGGAATGGCATGAYCATAGCTCCACTGCACCTCCTGG 5371
g o	AGAGGCAAGGTGGTAGGTAGAAACTCAGGAGTTCAAGACCAGCTGGGCAACACA	Qy 5372 GTTCA/ Db 15245 GTTCA	GTTCAAGCAAAGCTGTCGCCTCCAGCTCCCGGGTAGATGGGATTACAGGCGCCCACCACC 5431
ò g	GTGAAACTCCATTCTCCACAAAAATGGGAAAAAAAAGAAAG	Qy 5432 ACACTC Db 15305 ACGCCC	ACACTCGGCTAATGTTTGFATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGC 5489
8 & A	GGGGAGGGGAAGGACTGCAAAGAGGAAGAAGAGCTCTGGTGGGGGGGG	Oy 5490 TGGTC: Db 15365 TGGTC	TGGTCTCAAACTCCTGACCTCA 5511
Qy	4485 TCAGGITCTGTATCCTGACTGTGGTAGCAGTTTGGGGGTGTTTACATCCAAAAATATTCGT 4544	RESULT 12	

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ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                             Human digestive system antigen genomic sequence SEQ ID NO: 2994
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2000US-0180628.
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2000US-018974.
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                         AAK89418 standard;
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PRESENTATION OF STREET OF

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AATGTCCTCCACAAGGGAAACTGAAACTTATTGCTTGATAAGTGTCCTTTGGTTATAAA 20600
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment
                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \,
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Pred. No. 1.5e-28;
1; Mismatches 1142;
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Matches 1154; Conservative
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 anti-infertility
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   21381 TCAGGTGGAAAGAAGATAGACCTGGTCTCTACTGTTGTATTGCCTTCTAGTTTAGTGGATG 21440
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4773 CCAGGCATCACTTGTGCTTTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCAG 4832
                                                                                                                                            5162 GACACTATGATATTTGAGATTTAAAAATCTTTAATATTTTAAAATTTAGAGCTCTTCTA 5221
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                                                              4982 CAACATAGCAAGATATTTAGATCATTTTGACTAGTTAAAAAAGCAGCAGAGTACAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21141 GAATGGAAAAGCATTTCAAAAACGGAATGGCAGTTGCCCAGTTCCTGGAATCTAATCCTT
                                                                                               TTCCACAAATGCTATTCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated protein; human; mouse; rabbit; goat; horse; cat; dog;
                                              4833 CIGCAAIGGGGACTCTTGAITTCTTTAAGGAAACTIGGGTTACCAGAGTAI-----
                                                                                                                                                                                                                                          5042 ACACATGCAATCAGTATAATCCAAATCATGTAAATATGTGCCTGTAGAAAGACTAGAGGA
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Sequences AAS31827-AAS32182 represent genomic DNA molecules, which encode the liver associated polypeptides of the invention. Liver associated polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in equinoparious condition of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a liver associated polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as corneal infection, encourant disorders such as corneal infection, encourant disorders such as corneal infection, and ciscaders such as corneal infection, encourant disorders such as corneal infection, encourant disorders such as corneal infection, encourant disorders such as crown's disease, renal disorders such as solumer as also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                           Isolated nucleic acid molecule encoding a human liver related protein is used in preventing, treating or ameliorating disorders of the liver particularly cancer of the liver -
                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 399; 526pp; English.
                                                                              Ruben SM;
                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                 WPI; 2001-457728/49.
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19641 CTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCACCACCATGCCCAGCTAATTT 19700 19581 AGTGAAGTGGCGTGATCTCAGCTCAACCTCCACCTCCTGGGTTCAAGCGATTCTC 19640 19701 TTTATATTTTTAGTAGAGGGGTTTCACCGTGTTGACCAGGCTGGTCTCAAACTCCTG 19760 19761 ACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAAGTGTTGGGATTACAGGCATGAGCCAC 19820 19821 CGTGCCTGGCCAAAAAAATTTTTCTGATTTTAGAGGAAAGTGTTATAAAAATAGTTATT 19880 3333 CTGCCTTGGCCTCCCAAAGTGTTGGGAT---ACAGTCATGAGCCACTGCATCTGGCCTAG 3389 3390 GATCCATTTAGATTAAAATATGCATTTTAAATTTTAAAATATATAG----CTAATTTT 3445 3446 ACCTTATGTAAT-----GTGTATACTGGTAATAAATCTAGTTTGCTGCCTAAAGTTTA 3498 3553 GACAGCCAGGTGTGGTGGTTCACGCCTGTAATCCCAGCACTCTGGGAGGCTGAGGTGGGT 3612 3273 AGTGCAGTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTC 3499 AAGTGCTTTCCAATAAGCTTC-----ATGTACGTGAGGGGAGACATTTAAAGTGAAACA 3613 GGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAAACCCTGTTTCT 3213 TITATGTTTTTATGTTTTTGATTTTTAAAAGACAATCTCACCCTGTTACCCAGGCTGG 94; Gaps Query Match 4.1%; Score 225.4; DB 22; Length 28588; Best Local Similarity 48.3%; Pred. No. 1.5e-28; Matches 1154; Conservative 1; Mismatches 1142; Indels 94; 19881 qq ò g à Db ò g ò g ò g ò g

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3724 20060 3784 20120 3844 20180	3888 20240 3948 20300		4127 20480 4183 20540	4242 20600 4302 20660 4362 20720	4422 20780 4479 20840 4539	ATG 4599 AAG 20960 AAT 4659 AAT 21020 AAT 2102
ATAACAAA AATTAGCCGGGCATGGGCATGTGGCTGTGGTCCCAGCTACTA	AAAATTAAAAATGGAAACAACTACAAAGAGCTGTTGTTGTC 1111	CACCTGCACTACATTATTAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTAC		AGAGTCAGACATGAAGGAGATAATGTATGCCATACGAAAT-TCTAGAAAATGAAAGT		TTCGTAGAATTATGCATCTTAAATGGGTGGAGTTTACTGTATGTA
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New nucleic acid encoding human liver antigens, useful for diagnosis, treatment and prevention of e.g. hepatitis and hepatic cancer, also related polypeptides and antibodies
hepatotropic; cytostatic; antiinflammatory; virucide; antibacterial; fungicide; parasiticide; antidote; immunosuppressive; gene; ds.
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RUBEN S M.
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The invention relates to 145 novel human liver antigens (ABP40831-ABP40975) and to cDNAs encoding them (ABN90036-ABN90180), and also encompasses polypeptides 90% identical and polypucleotides 95% identical comprision additionally relates to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human liver antigen

CC polynucleotides, antibodies against human liver antigens, and the use of liver antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various disorders of the liver. Such conditions (c.g., clonorchis sinenis, Echinococcus granulosus and confidential infections (e.g., cytomegalovirus, Epstein-Barr virus, hepatitis A virus, hepatitis B virus and hepatitis C virus), parasitic infections (e.g., clonorchis sinenis, Echinococcus granulosus and cisorders that may be treated include inflammatory conditions (e.g., cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins, autoimmune diseases (e.g., Wilson's disease, primary biliary cirrhosis, carcinoma), portal hypertension, or gastrointestinal disorders (e.g., poptic ulcers, gastritis and peritoneal diseases). Liver antigen compounds which modulate liver antigen expression or activity. The polypeptides may further be used for gene therapy, chromosome compounds which modulate liver antigen expression or activity. The phenotyphing, sequences ABN90182-ABN90537 represent human liver antigen comming comming expression or prepare antibodies useful in disease diagnosis, drug targeting and comming expression or activity concerned and penipones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3390 GATCCATTTAGATTAAAATATGCATTTTAAAATTTATAAAATAATATGG----CTAATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 225.4; DB 24; Length 28588;
Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28588 BP; 7983 A; 5600 C; 5729 G; 9276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches 1142; Indels
                      Disclosure; SEQ ID No 399; 181pp; English.
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20001 ACCAAAAATACAAACCAATTAGCCAGGTGCAGTGGCATGTGCCTGTGGTCCCAGATACTC,20060
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                                                                                                                                                                                     GGGGGCTGAGGCAGGAGATCTTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAGTGCT
                                                                                                                        3949 CACCTGCACTACATTATAAAATATCAATTCTCAATGTATATCCACACAAAGACTGGTAC
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                                                                   4884 TTCCACAAATGCTATTCAAATTAGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAG
                                                                                                                            TITCAGCAGITATCCTGAGCATCGTGTTATGTAACATTTATTTGTAAGTTAGGTGCTTT
                                                                                                                                                    4944 AAAACAAAGAGGAGAAAATCAGTCATTA----------TGTGGGAA
                                                                                                                                                                           21321 CACGTATTGTTTTTTTTTTTTTTTTTTTGAGCACTGCCATGTTCAGGCTCTGTGGTGG
                                                                                                                                                                                                      CAACATAGCAAGATATTTAGATCATTTTGACTAGTTAAAAAAGCAGCAGAGTACAAAATC
                                                                                                                                                                                                                              21381 TCAGGTGGAAAGAAGATAGACCTGGTCTCTACTGTTGTATTGCCTCTAGTTGGTGGATG
                                                                                                                                                                                                                                                      5042 ACACATGCAATCAGTATAATCCAAATCATGTAAATATGTGCCTGTAGAAAGACTAGAGGA
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                                                  4833 CTGCAATGGGGACTCTTGATTTCTTTAAGGAAACTTGGGTTACCAGAGTAT
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. 1000-MAT-51 3	NAD-11	31-JAN 04-FEB	24-FEB-2000	02-MAR-2000	17-MAR-2000	8-APR-2000	9-MAY-2000	7-JUN-2000	8-JUN-2000	0-JUN-2000	7-JUL-2000	7-JUL-2000	1-JUL-2000	1-JUL-2000	4-JUL-2000	6-JUL-2000	6-JUL-2000	4 - AUG - 2000	4 - AUG - 2000	4 - AUG - 2000	14 - AUG - 2000	4 - AUG - 2000 4 - AUG - 2000	4 - AUG - 2000 4 - AUG - 2000	4 - AIIG - 2000	14-AUG-2000	14-AUG-2000	4 - AUG - 2000	4 - AUG - 2000	8-AUG-2000	2-AUG-2000 2-AUG-2000	2-AUG-2000	2 - AUG - 2000 3 - AUG - 2000	0-AUG-2000	1-SEP-2000	1-SEP-2000	1-SEP-2000	1-SEP-2000	5-SEP-2000	5-SEP-2000	6-SEP-2000	8-SEP-2000	8-SEP-2000	8-SEP-2000	8-SEP-2000 8-SEP-2000	8-SEP-2000	8-SEP-2000	2-SEP-2000	4-SEP-2000	14-SEP-2000	14-SEP-2000	4 - SEP - 2000 4 - SEP - 2000	4 - SEP - 2000	4-SEP-2000	4-SEP-2000	1-SEP-2000	I-SEP-2000	5-SEP-2000 5-SEP-2000	6-SEP-2000	7-SEP-2000	7-SEP-2000	9-SEP-2000	9-SEP-2000	9-SEP-2000	9-SEP-2000	

SM; 20000S - 023690 20000S - 0237037 20000S - 0237037 20000S - 0237039 20000S - 0237039 20000S - 0241785 20000S - 0241786 20000S - 0241786 20000S - 0241809 20000S - 0241809 20000S - 0241809 20000S - 0241806 20000S - 024677 20000S - 0246528 20000S - 0246529 20000S - 0246529 20000S - 0246528 20000S - 0249208 20000S - 0249218 Ruben 2000US-0251479. 2000US-0251856. 2000US-0251868. 2000US-0251869. HUMAN GENOME SCI INC 2001US-0259678 Barash SC, 29-SEP-2000)
02-OCT-2000)
02-OCT-2000)
02-OCT-2000)
03-OCT-2000)
03-OC 08-DEC-2000; 05-JAN-2001; Rosen CA, (HUMA-)

Isolated nucleic acid molecule encoding a reproductive system antigen

WPI; 2001-465570/50

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAAACCCCTGTTTCTATAACAAAA 3681
                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                CAATCCTCCTGCCTTGGCCTCCCAAAGTGTTGGGA-TACAGTCATGAGCCACTGCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5746 ATTACAGGCATGAGCCAC----CATGCCCGGCCAACTTTTATTTTTAAAAGTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTAATTTTTTGTATTTTAGTACAGACAGGGTTACACCGTGTTAGCCAGGGTGGTCTCG
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                                                                                                                                                                                      Gaps
 is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                         Score 221.6; DB 22; Length 10855;
Pred. No. 6.1e-28;
0; Mismatches 219; Indels 20;
                        Disclosure; SEQ ID NO 7965; 1297pp + Sequence Listing; English.
                                                                                                                                 Sequence 10855 BP; 2779 A; 2798 C; 2683 G; 2595 T; 0 other;
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Local Similarity 63.9%;
hes 423; Conservative
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum Maximum Database

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AQ743399 HS_5387_B
AU118632 AU118632
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B0673918 AGENCOURT
BF897850 QVI-MT022
BM768638 K-EST055
AQ807427 HS_3177_A
AQ807427 HS_3177_A
AQ807427 HS_3177_A
AQ807427 HS_3177_A
AQ807427 AGENCOURT
BG670979 AGENCOURT
BG670979 AGENCOURT
BG7727 7 AG2210.x
AQ75268 AV755268
AQ75367 HS_5073_B
AQ80303 CR5211-2
BQ188600 UI-E-EJ1-2
BQ188600 UI-E-EJ1-2
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AG18665 AGRNCOURT
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CIT-HSP-2326M11.TR CIT-HSP Homo sapiens genomic clone 2326M11, DNA
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other GSSs: CIT-HSP-2326M11.TV
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Email: mddadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS
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AQ046391 RPCIII-35
BG941633 ax15609.x
BM990649 UI-H-DIO-
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12010.756 Million cell updates/sec
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                                                                                       June 18, 2003, 23:34:44; Search time 7435.16 Seconds
                                                                                                                                                                                                                                                                     32308132
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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AQ045714
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Pan troglodytes
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: M13 Reverse
Class: BAC ends.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totokl,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fullyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Pan troglodytes DNA, clone: PTB-028H18.F, genomic
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Pred. No. 7.5e-23;
0; Mismatches 1; 1
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                                                        1. .293
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2326M11"
/clone_lib="CIT-HSP"
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                                           Location/Qualifiers
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Eukaryota: Metazoa: Chordata: Cranlata; Vertebrata: Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. I (bases 1 to 373)

13. Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

13. Upublished (1998)

14. Upublished (1998)

15. Upublished (1998)

16. Upublished (1998)

17. Medical Reveryotic Genomics

18. The Institute for Genomic Research

19. Medical Center Dr., Rockville, MD 20850, USA

19. The Institute for Genomic Research

19. The Institute for Genomic Research

19. Medical Center Dr., Rockville, MD 20850, USA

19. Tal: 301 838 0208

19. Email: mdadams@tigr.org

10. Clones are derived from the human BAC library RPCI-II. For BAC

10. Ibrary avallability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu)orgenical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3552 AGACAGCCAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGGAGGCTGAGGTGGG 3611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3786 GCGCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTTGCCTCAAAAAAATAAGAAGA 3845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3612 TGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGGCAAAACCCTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3672 T-----ATAACAAAATTAGCCGGGCATGTGGCATGTGCCTGTGGTCCCAGCTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3726 GGGCCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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9
                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 199.4; DB 17; Length 694;
81.2%; Pred. No. 4.1e-13;
tive 0; Mismatches 51; Indels 6;
                                                                                                                                                                                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
206 c 157 g 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .694 //
/organism="Pan troglodytes"
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/clone="PTB-028H18.F"
/sex="male"
                                                                           Location/Qualifiers
: pKS145
: SacI
: SacI.
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AQ045714
AQ045714.1 GI:3314641
GSS.
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R.Site 2
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es 246; Conserv
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Gaps

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BG941633 throliferating Human Erythroid Cells (LCB:ax library) ax15d09 throno sapiens cDNA clone ax15d09 random, mRNA sequence. BG941633.1 GI:14341005
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Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 403)
Gene expression in proliferating human erythroid cells
Genemics 59 (2), 168-177 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jm/femin.gov analyses by National Institutes of Health DNA Sequencing and analyses by National Institutes of Health DNA Sequencing and center (NISC).

Intramural Sequencing Column: 09

Plate: 15 row of Column 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 CAGGTGGAGTGCAGTCTTGGCTCACTGCAACCTCCAACTCTGGGTTCAAG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5259 TIACTCITTICITTITTITTITTITTITTITTITTICAGATGGAGTTITTGCTCTTGTTGCC 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .400
/organism="Homo sapiens"
/db_xref="GDB:7513156"
/db_xref="taxon:9600"
/db_xref="taxon:9600"
/db_xref="taxon:9600"
/clone="record record recor
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC_ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Score 199.2; DB 17; Length 3.6%; Pred. No. 6.3e-13; Best Local Similarity 86.2%; Pred. No. 6.3e-13; Andels Matches 219; Conservative 1; Mismatches 19;
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                                                                                                               Location/Qualifiers
1. .408
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Fax: 301 435 5148
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases, 1 to 408)
Adams, M. D., Rounsley, S. D., Zhao, S., Field, C. E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C.
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                                                                                                                                                    Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.btml
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male" Lymphocytes" | Site_1: EcoRI; Site_2: EcoRI; /cell_type="Lymphocytes" | Site_1: EcoRI; /note="vector: pBaCe3.6; Site_1" | Note="vector: pBaCe Library" | RPCILI Human Male BAC Library" | RPCILI Human Male BAC Library | R3 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                     /, organisme"Homo sapiens"
/dp_xrefe"GDB:7513062"
/db_xrefe"taxon:9606"
/db_xrefe"taxon:967"
/clone="RPCI-11"
/clone_llb="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQQ46391.1 GI:3315318
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Query Match
Best Local Similarity 86.2%;
Best Local 219; Conservative 1
Matches 219;
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AQ046391
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ORIGIN
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/note="Organ: blood; Vector: Lambda ZAP II; Site_1: ECORI; Site_2: ECORI; 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIZOI reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manutacturer's protocol and cloned into ECORI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the CDNA inserts were sequenced in high thtp://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM990649 689 bp mRNA linear EST 17-JUN-2002
UI-H-DIO-atp-o-13-0-UI.s1 NCI_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5862756 3', mRNA sequence.
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                                            'clone_lib="Proliferating Human Erythroid Cells (LCB:ax
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                                                                                                                  /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 403;
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Pred. No. 1.3e-12;
1; Mismatches 32; Indels
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
/db_xref="taxon:9606"
/clone="ax15d09"
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                                                                                              "sex="unknown"
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ilarity 86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Email: cgapbs-r@mail.nih.gov

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/organism="Homo saplens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3281 GGTGCAATCATAGCTTTCTGCAGTCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTTG 3340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3400 GATTAAAATATGCATTTTAAATTTTAAATAATATGGCTAATTTTTACCTTATGTAATGT 3459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3580 GTAATCCCAGCACTCTGGGAGGCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGA 3639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3640 CCAGCCTGAGCAACATGGCAAAACCCTGTTTCTATAA-----CAAAAATTAGCCGGGCA 3693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CATAACCT -- TGTCTCTACTAAAAGTGCAAAGATCGGCCAGGAGTGATGGCACATGTCT 357
                                CDNA Library preparation: Dr. M. Bento Soares, University of lowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this CDNA sequence: 11-168, >ALU (matched compliment) 199-418, >ALU 334-623, >ALU 634-661, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3520 ATGTACGTGAGGGAGACATTTAAAGTGAAACAGACAGCCAGGTGTGGTGGCTCACGCCT
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Pred. No. 9.6e-13;
0; Mismatches 256;
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TAG_SEO-ATACGCGGTC"
161 c 170 g 168 t
issue Procurement: Dr. Jose Mercuende
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Best Local Similarity 60.0%
Matches 400; Conservative
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Homo sapiens clone FLC0578 PRO2852 mRNA, complete cds.
AF130079
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Zhang,C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y.,
Xu,W., Gao,F., Liu,M. and He,F.
Functional prediction of the coding sequences of 75 new genes
deduced by analysis of cDNA clones from human fetal liver
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FLVETGFHHIGQAGLELLTSGDPPAWASQSAGITGVSHCARLVCACCIKFGKSFFAAR
HVVLINTVVYLSIMMYISSDIYFQYLLDYKGRLLRSCFLIIFGVIGPQGFKRRLDCAL
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(bases 1 to 1769)

Zhang, C., Yu, Y., Zhang, S., Wei, H., Bi, J., Zhou, G., Dong, C., Zai, Y.,
Direct Submission
                      5263 TCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTTGGTCTTGTTGCCCATG 5322
                                                                                                                                                                              5383 GCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCCACCACCACACTCGGCTA 5442
                                                                                                                         199 CTGGAGTGCAATGGCACGATCTCGGCTAACTGCAACCTCCGCCTCCCGGGTTCAAGCGAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           139 TCTCCTGCCTCAGCTCTCGAGTAGCTGGGATTACAGGCCATGCGCCACCATGCTGGCTA
                                                                                                  CTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAA
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/product="PRO2852"
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/note="predicted protein
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/db_xref="taxon:9606"
/clone="FLC0578"
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/rpt + +----
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complement(627. .938)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="liver"
/dev_stage="fetus"
complement(338. .513)
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683. .1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pcMv-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGGGGCCGCCG-3' and
5'-GACTAGTTCTAGATCGCGAGGGGCCGCCCT(15)-3'. Size selected >
1kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor COLlege of Medicine) and is available through Life
                                                           TGGTGGCATGTGCCTGTGGTCCCAGCTACT-AGGGGGCTGAGGCAGGAGAATCTTTGGAG 3752
                                                                                                                                     3753 CCCAGGAGGTCAAGGCTGCACTGAGCAGTGCTTGCGCCACTGCACTCCAGCCTGGGTGAC 3812
                                                                                                                                                                                                                     ö
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13612 row: d column: 15
High quality sequence stop: 614.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 9.7e-13;
1; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:6199262"
/clone_lib="Lupski_sciatic_nerve"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ932123.1 GI:22347154
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Best Local Similarity 86.0%;
Matches 215; Conservative
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86.38;

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Best Local Similarity
Matches 214; Conser
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1027)

NIH-MGC http://mgc.ncl.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MCC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov
Plate: LLCMASSIZ row: o column: 11
                                                                                               5470
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                                                                                                                                                 5351 ACTGCAACCICCACCICCTGGGTTCAAGCAAAGCTGTCGCCTCAGCCTCCCGGGTAGAIG 5410
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                                                                 GGATTACAGGGGCCCACCACCACACTCGGCTAATGTTTGTATTTTTAGTAGAGGTGGGGT
                                                                                                                                                                                                                 BG539940 1027 bp mRNA linear EST 03-APR-602567448F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692322 5'
                               Gaps
                               ;
     DB 11; Length 1769;
                              Indels
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Pred. No. 5.9e-13;
1; Mismatches 54
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High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG539940
BG539940.1 GI:13532173
 tch 3.5%;
al Similarity 80.5%;
227; Conservative
Query Match
Best Local Similarity
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Score 194.8; DB 12; Length 1027;

3.5%;

Query Match

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/organisme"Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6272500"
/clone="IMAGE:6272500"
/clone="type="epidermoid carcinoma, cell line"
/lab_host="All08 (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTH7; Site_1: XhoI: Site_2: EcoRI: cDNA made by oligo-dT prining.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using XAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISM Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases I to 1016)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

INDUDIIShed (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM2450 row: p column: 05

High quality sequence stop: 515.

Location/Qualifiers

Loure I. 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT_8414352 NIH_MGC_102 homo saplens cDNA clone IMAGE:6272500 5', mRNA sequence.
BQ674146
BQ674146.1 GI:21784980
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                                                                   5265 TTTCTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGCCCATGCT
                                                                                                                                                                  5325 GGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAAAGC
                                                                                                                                                                                                                                                                                                     189 TCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCGCCACCATGCCTGGCTAAT
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Pred. No. 9.7e-13;
1; Mismatches 33;
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85.0%; Pred. No. 1.1e-12;
tive 1; Mismatches 37;
                       1;
                       Conservative
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Best Local Similarity 85.0
Matches 216; Conservative
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GACCTCAG 62
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 532)

2 taoo, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building

Unpublished (1997)

Other_GSSs: CITHLE1-2529E11.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.
                                                                                                                                                                                          5359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ356384 1inear GSS 24-JAN-1999
CITBI-E1-2529E11.TR CITBI-E1 Homo sapiens genomic clone 2529E11,
                                     5180 ATTTAAAAATCTTTAATATTTTAAAATTTAGAGCTCTTCTATTTTTCCATAGTATTCAA 5239
                                                                                                                                                                                                                                                                   5360 TCCACCTCCTGGGTTCAAGCAAAGCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAG 5419
                                                                                                                                                                                                             240 TCCACCTCCCGGGTTCAAGTGATTCTCCTGTCTCAGCCTCCTGAGTAGCTGGGATTACAG 181
480 ACANACATCCAGAATATCTTCTACTTCAGAGTATCTTCCAAATGTATAAGTTAAAC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Site_2: EcoRI;
                                                       180 GCACCTGCCACACACCACACCACACTATTTTGTATTTTAGTAGAGATGGGGTTTCACCATG
                                                                                                                                                                                                                                                                                                                                            5420 GCGCCCACCACCACACACTCGGCTAATGTTTGTATTTTTAGTAGAGATGGGGTTTCACCATG
                                                                                                                5300 GAGTTTTGGTCTTGTTGCCCATGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACC
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/note="Vector: pBeloBAC11;
CalTech Human BAC Library D
a 134 c 110 g 185 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
/sex="male"
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                   5318
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                                                                                                                                                                  5379 CAAAGCIGICGCCICAGCCICCGGGIAGAIGGGAITACAGGCGCCCACCACCACACTCG 5438
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Adams,M.D. and
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                                                                                         5319 CATGCTGGAGTGGAATGGCATGAYCATAGCTCACTGCAACCTCCACCTCCTGGGTTCAAG 5378
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                                                                                                              206 GCTAATTTTTGTATTTTTAGTAAGATGGGGTTTCACCATGTTGGTCAGGCTGGTCTAA 265
                                                       82
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Elmail: jwallace@u.washington.edu
Elmail: jwallace@u.washington.edu
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3051 row: C column: 10
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
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                 TTACTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCC
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                                 /clone_lib="CIT Approved Human Genomic Sperm Library
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref-"taxon:9606"
/clone-"Plate=3051 Col=10 Row=C"
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Location/Qualifiers
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Class: BAC ends
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AQ734866/c
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BF575954/c
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TITLE
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/clone="IMAGE:5863584"
/clone="IMAGE:5863584"
/clone=lib="NCI_CGAP_FS1"
/tissue_type="Fibrosarcoma"
/tab_host="PH108 [Life Technologies)"
/note="Vector: pT773-Pac (Pharmacia) with a modified
polylinker; Site_1: ECOR 1; Site_2: NOt 1; NCI_CGAP_FS1 is
a cDNA library containing the following tissue(s):
Fibrosarcoma Cell line HT-1088 (ATCC number CCL-121). The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
                                             5322
                                                                                                                                                                                                                                                                                                  BM989249 451 bp mRNA linear EST 17-JUN-2002 UI-H-DP0-ats-b-01-0-UI.sl NCI_CGAP_Fsl Homo sapiens cDNA clone IMAGE:5863584 3', mRNA sequence.
    ö
                                                                                                                           5323 CIGGAGIGGAAIGGCAIGAYCAIAGCICACTGCAACCICCACCICCIGGGIICAAGCAAA 5382
                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA Sequencia Dy: Dr. M. Bento Soares, University of Iowa
DNA Sequencia Dy: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this CDNA
compliment)
                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 451)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                          5263 TCTTTCTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTTGGTCTTGTTGCCCATG
                                                                                                                                                    5383 GCTGTCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCACCACCACCACACTCGGCTA
      Gaps
  ;
0
  34; Indels
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM989249.1 GI:19708638
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Unpublished (1997)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                          CTGACCTCA 5511
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BM989249
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885 bp mRNA linear EST 12-DEC-2000
MRNA sequence.
BF575954
BF575954.1 GI:11649666
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                                                                                                                                                                                                                                                                                                                                                                                                                                              230 TGCAATGGCGCCATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGCGATTCTCT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:4288254"
/clone=lib="NIH_MGC_81"
/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/gccattatggco; Site_1: SfiI (ggcgcctcggcc); Site_2: SfII
(glocattatggco); S and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCCGACATG-dT(30)BN-3' (where B - A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8015)
NIH-WGC http://mgc.ncl.nih.gov/.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1127 row: k column: 07
High quality sequence stop: 302.
Location/Qualifiers
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                                                                                                                                                                                                                                                   Gaps
site and the (dT)18 tail. The sequence tag for this library is GTCTACGAG.
TAG_LIB-UT.+DPO
TAG_LIB-Eibzosarcoma
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Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                Score 194; DB 14;
Pred. No. 2.1e-12;
1; Mismatches 31;
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                                                                                              TAG_SEQ=GTTCTACGAG"
111 c 82 q
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ilarity 86.9%;
Conservative
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212; Conserv
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3818
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availablity, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu). clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) trtp://www.htsc.washington.edu
Seq primer: 596
Seq primer: 596
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C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length colones and was constructed by Clontech Laboratories (Palo Alto, CA). 253 g 108 t
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                               Query Match 3.5%; Score 194; DB 12; Length 885; Best Local Similarity 85.3%; Pred. No. 1.3e-12; Matches 215; Conservative 1; Mismatches 36; Indels
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/organism="Homo sapiens"

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/clone_lib="RPCI-11 Human Male BAC Library"
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/clone_lib="RPCI-11 Human Male BAC Library"
/mote="Wetor: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Mathylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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/db_xref="taxon:9606'
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICKNENT EPITHELUM
TITLE OF INVENTION: BICLOGICAL ACTIVITY AND SEQUENCES ENCODING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
WUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   Sequence 10
Sequence 4,
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US-09-798-096-10
US-09-750-580-1
US-09-268-992-7
US-09-268-992-7
US-09-37-474-7
US-09-345-882-10
US-09-270-542-101
US-09-270-542-101
US-08-370-542-101
US-08-38-136-2
US-08-658-136-1
US-08-658-138-1
US-08-814-095-7
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                         US-08-257-963B-9/c; Sequence 9, Application US/08257963B; Patent No. 5840686
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
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MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Human
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CITY: New York
STATE: New York
COUNTRY: USA
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LENGTH: 4421 Base Pairs
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Sequence 3 Sequence 3 Sequence 3

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Sequence Sequence 6

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1; Mismatches 995;
IDENTIFICATION METHOD:
OTHER INFORMATION: 7.1 kb Bam HI
OTHER INFORMATION: fragment Derived from
OTHER INFORMATION: genomic DNA
                                                      4.0%; Score 218.6;
47.7%; Pred. No. 6.8e
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                                                                 Similarity
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                                                           Sequence 9, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 4421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment Derived from human placental genomic DNA; Also referred to as JT101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 218.6; DB 4;
Pred. No. 6.8e-37;
1; Mismatches 995;
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy Disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202641260S2
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APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1 kb Bam HI
                                                                                                                                                                                                                                                  STREE: Morgan & Finnegan STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGHH: 4421 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
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REFERENCE/DOCKET NUMBER: 2
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Best Local Similarity 47.7%;
Matches 952; Conservative
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OTHER INFORMATION: fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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                                           US-08-367-841A-9/C
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3747 AGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATCCAGACCATCCTGGCTAACACGGTGA 3688
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                                                                                                                                                                                                                                                                                                                                                              Length 4421;
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Pred. No. 6.8e-37;
1; Mismatches 995;
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: CDS 66-322
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.7%;
Matches 952; Conservative
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APPLICANT: Steele, Finten R
APPLICANT: Combran-Tink, Joyce
APPLICANT: Steele, Finten R
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Bochieve, Ignacio R
APPLICANT: Rodriguez, Ignacio R
ITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR FILE REFERENCE: 2026-4203US1
CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-01-25
PRIOR FILING DATE: 1995-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2570 ATAIGGAGCCGITITATIGAGCAGITICCICCAGGGAIGACGGCTGTCAGTGTGTTCCT
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                                                                     CATCACTTGTGCTTTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCAGCTGCA
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3928 3769 3868 3829 us-09-966-880a-9.rni

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TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIYED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
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fragment Derived from human placental
genomic DNA; Also referred to as JT10
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                                                                                                                                                                                                                                                                 APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 218.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:

    Morgan & Finnegan, L.L.P.
    Park Avenue

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FILING DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy Disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM PC-DOS/MS-DOS SOFTWARE: WORDPERPECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             PCT-0S95-07201-9/c; Sequence 9, Application PC/TUS9507201; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
                                                                                                                           2154 AACTCCCGGCCTCAG 2140
                                                                                                          AACTCCTGACCTCAG 5512
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
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OTHER INFORMATION:
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MOLECULE TYPE: Geno
ORIGINAL SOURCE:
ORGANISM: Human
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                                                                                                                                                                                            ATTC----AGGTTCTGTATCCTGACTGTGGTAGCAGTTTGGGGGTGTTTACATCCAAAAA 4537
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4423 TCCTGTGGGGAGGGGAAGGACTGCAAAGAGGGAAGAAGTCTGGTGGGGGTGAGGGTGGTG
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Length 4421;

as JT101

Best Loc Matches	Local Similarity 47.7%; Pred. No. 6.8e-37; hes 952; Conservative 1; Mismatches 995; Indels 47; Gaps 9;	qq	
Qy	3538 ATTIAAAGTGAAACAGACAAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGG 3597	۸ŏ	
qq		q	
0y	3598 GAGGCTGAGGTGGGTGGATCGCTTGAGCCCTGGAGTTCAAGACCAGCCTGAGCAACATGG 3657	Oy.	
qq	4047 GAGGCTAAGGTGGGCGGATCACCTGATGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG 3988	g G	
ογ	3658 CAAAACCCTGTTTCTATAACAAAATTAGCCGGGCATGGTGGCATGTGCCTGT 3710	ογ	
qa	3987 TGAAACCCCATCTITACTAAAAATACAAAACTAGCCAGGCGTGGTGGTGGTGGGCCACCTGT 3928	qa	
٥y	3711 GGTCCCAGCTACTAGGG-GGCTGAGGCAGGAGAATCTTTGGAGCCCAGGAGGTCAAGGCT 3769	Qy	4778 CATCACTTG1
qq	3927 AATCCCAGCTACTIGGAGGCTGAGGCAGGAGAATCTCTTGAACCCAGGAGGCGGAGGTT 3868	qa	
ογ	. 3770 GCACTGAGCAGTGCGTTGCGCCACTGCACTCCAGCCTGGGTGACAGGACCAGACCTTGCCT 3829	0y	4838 ATGGGGACTC
ΩĐ	3867 GCAGTGAGCCGAGATCGCTCCACTCCAGCCCAGGTGACAGTGAGACTCCATCT 3808	qa	2810 CTCAGTGATC
٥y		Qy	
qq		qа	2750 GIGCACCAC
δλ		Qy	4958 GAGAAATCAC
q		qa	2690 ATAAAACAAC
ò	CACCTGCACTTATTAAAATATCAATTCTCAATGTATATCCACACACA	Oy	5018 AAAAAAGCAG
7 G		qa	2630 TCTAGCTTCC
ò	GTGAATGTTCATAGTACCTTTATTCACAAAACCCCAAAGTAGAGAGTTCATAAACCCCAAAAGTAGAGAGAG	QY	5078 TGTGCCTGT
7 q	GCCGTGCTGCCGACCTCACACCTACTCGCAGGTTGAGGCAGAAATGGGG	qa	2570 ATATGGAGCC
ò	TCAACAAGTGAACAAATAAACAAAATGTGCTATATCCATGCAATGGAATACCACCTGCA	Qy	5138 CACTAAGTC1
· 6		qq	2510 GCCAGTTTTC
γo		Qy	5198 ATTTTAAAA1
· q		qq	2450 CAACCACTA
ò	CAGACATGAAGGAGGAGATAATGTATGCCATACGAAATTCTAGAAAATGAAAGTAAC	Qy	5258 ATTACTCTT1
qq	ATGTGGGTTCTGTGGGTTCTGTGGGTTCTGTGGGTTCTGCAG	qq	2393 TGAGTTGTTC
^0	TTATAGTTACAGAAAGCAAATCAGGGCAGGCATAGAGGGTTCACACGTAAATCCCAGG	٥y	5318 CCATGCTGG
. q	GTGCCGATTCTGTAGGTTCTGCAGGCCCAGGTAAACCTGTAATCCCAGT	QQ	2333 CCAGGCTGG
οy		Qy	5378 GCAAAGCTG1
qq		qa	2273 GTGATTCTCC
'n	AACACAGTGAAACTCCATTCTCCAAAAATGGGAAAAAAAA	δλ	5438 GGCTAATGT1
ු අ		qq	2213 GGCTAAT-TI
δŏ	TCCTGTGGGGAGGGAAGGACTGCAAAGAGGGAAGAAGCTCTGGTGGGGTGAGGTG	ΟŊ	5498 AACTCCTGAC
ΟD		qq	2154 AACTCCCGGC
δŷ	4483 ATTCAGGITCTGTATCCTGACTGTGGGAGCAGTTTGGGGGTGTTTACATCCAAAAA 4537	RESULT	5
qa	3170 AGGCIGCAGTGAGCCAAGATGGCACTACTGCAGCCTGGGTGACAGAGTAAGACCC 3111	Seque	05-06-724-3948-20/C ; Sequence 20, Applicati . Patont No. 507327
Qy	4538 TATTCGTAGAATTATGCATCTTAAATGGGTGGAGTTTACTGTATGTA	GEN	ent no. 38/223/ NERAL INFORMATION: APPLICANT: Feder.

SCCCTTTACTTCGCAAATTCTCTGCACTTCTGCCCCGTACCATTAGGTGACA 4717 rccacaaattggataaatgcatttctggaaaagactagggacaaaatccagg 4777 2871 2811 4957 5017 5077 5137 2511 5197 2451 5257 2394 5317 5437 2214 CAAAAAAATAACAGGTTCTGTTGCTGCTGAGCTTTCGTCAGGAAGATAAGAC 3051 AAAATAATGTGTAAGAAAAGTTTCAATTCTCTTGCCAGCAAACGTTATTCAA 4657 STGCTTTCATATCAACCACGCTGTACAGCTTGTGTTGCTGTCTGCAGCTGCA 4837 ICTIGATITICITTAAGGAAACTIGGGTTACCAGAGTAITTCCACAAAIGCTA 4897 IGATAGTCTGTTTCCCTGGAACATTCCTGTGGTTTTAGTAGTAATGAGATGT 2751 CCTCGACTCCTTTGTTAAAATCGTGGAGTATGAACTGTGACCAGAGAAGTAA 2571 ITTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCA 5497 CTCCAGTGGGAACTGAAGCTCTTAGTAGTTACATTGTAATTAAAAAGAATT 2691 AGAAATCAGCAAGCCTGCTTACCTCCAGAGACACGCGTTCCACTTACAGTA 2631 **AGCAGAGTACAAAATCACACATGCAATCAGTATAATCCAAAATCATGTAAATA IAGAAAGACTAGAGGAATAAACACAAGAATCTTAAACAGTCATTGTCATTAGA CTAATTATTATTATTAGACACTATGATATTTGAGATTTAAAAAATCTTTAAT ATTTAGAGCTCTTCTATTTTCCATAGTATCAAGTTTGACAATGATCAAGT** AATAAAATC---AAAGTTGTAGTAAAGACTTTATAACACATATGCCTCCTTC STCGCCTCAGCCTCCCGGGTAGATGGGATTACAGGCGCCCCACCACCACACTC **ACCTATITIGGTGAATATITITIGAAATAGTTAAGTGGCCTCCAGTACAAAC** AGTGCTTATGATATGCAAGACACTGTGCTAGGAGCCAGAAAACAAAGAGAG AGTCATTATGTGGGAACAACATAGCAAGATATTTAGATCATTTTGACTAGTT Lion US/08724394A ACCTCAG 5512 I: ', John N.